

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: July 24, 2001, 16:25:49 ; Search time 21.01 Seconds

(without alignments)  
3516.864 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 5116

Sequence: 1 LLAAVEETLMDSTTATAEELG.....ILNSTQVRAQMNIQSYEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68:\*\*

1: p1r1:\*\*  
2: p1r2:\*\*  
3: p1r3:\*\*  
4: p1r4:\*\*

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5112	99.9	970	2	receptor protein-t
2	4950.5	96.8	995	2	embryo kinase 5 -
3	3914.5	76.5	984	2	protein-tyrosine k
4	3754	73.4	985	2	receptor tyrosine
5	3707	72.5	952	2	protein-tyrosine k
6	3649.5	71.3	988	2	protein-tyrosine k
7	3632.5	71.0	998	2	protein-tyrosine k
8	3604	70.4	993	2	mouse developmenta
9	3429	67.0	938	2	protein kinase - m
10	3060.5	59.8	985	2	receptor tyrosine
11	3031	59.2	986	2	receptor protein-t
12	3031	59.2	991	2	receptor protein-t
13	3026	59.1	986	2	receptor protein-t
14	3016	59.0	998	2	receptor protein-t
15	3001	58.7	998	2	receptor tyrosine
16	2990	58.4	1013	2	receptor tyrosine
17	2930	57.1	981	2	receptor-like tyro
18	2918.5	57.0	983	2	receptor-like tyro
19	2914	57.0	983	2	receptor tyrosine k
20	2904	56.8	1005	2	receptor tyrosine
21	2875.5	56.2	983	2	receptor tyrosine
22	2835.5	55.4	987	2	mouse developmenta
23	2827.5	55.3	987	2	protein-tyrosine k
24	2792.5	54.6	987	2	eph-related recept
25	2714.5	53.1	849	2	protein-tyrosine k
26	2600	50.8	948	2	receptor-like tyro
27	2512	49.1	998	2	receptor tyrosine
28	2493	48.7	893	2	receptor-like tyro
29	2471	48.3	478	2	protein-tyrosine k

30	2466.5	48.2	480	2	148760	protein-tyrosine k
31	2442	47.7	877	2	148967	brain-specific kin
32	2438	47.7	1006	2	JC5526	kinase-defective E
33	2349.5	45.9	976	2	A36355	protein-tyrosine k
34	2340.5	45.7	977	2	S49004	tyrosine kinase Mp
35	2260.5	44.2	975	2	148974	receptor protein t
36	2246	43.9	612	2	S33506	tyrosine kinase re
37	1923.5	37.6	1019	2	T13039	protein-tyrosine k
38	1856.5	36.3	984	1	A34076	protein-tyrosine k
39	1548	30.3	490	2	I50613	receptor tyrosine
40	1477.5	28.9	605	2	JC5673	receptor tyrosine
41	1470	28.7	610	2	I48612	developmental kina
42	1467.5	28.7	626	2	I48614	developmental kina
43	1422	27.8	1122	2	T42400	Eph receptor tyros
44	1329	26.0	426	2	I48759	protein-tyrosine k
45	1252.5	24.5	919	2	T29581	hypothetical prote

## ALIGNMENTS

RESULT 1  
178842  
receptor protein-tyrosine kinase - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 18-Jun-1999  
C:Accession: 178842  
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch  
Oncogene 10, 897-905, 1995  
A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein  
A:Reference number: I58351; MUID:95206782  
A:Accession: 178842  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-970 <RES>  
A:Cross-references: GB:L36643; NID:9551609; PIDN:AAA7424.1; PID:9551610  
C:Genetics:  
A:Gene: HEK5  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea  
F:603-871/Domain: protein kinase homology <KIN>  
F:894-960/Domain: SAM homology <SAM>

Query Match	Score	5112	DB 2	Length	970
Best Local Similarity	99.9%				
Pred. No. 16-233					
Matches 969	Conservative	0	Mismatches 1	Indels	Gaps
0					
QY	1	LLAAVEETLMDSTTATAEELGMMVHPSPGMEVSGYDENNTTITTYOVCNVFESSQNNMLR	60		
DB	1	LLAAVEETLMDSTTATAEELGMMVHPSPGMEVSGYDENNTTITTYOVCNVFESSQNNMLR	60		
QY	61	TKTIRRGARHRIHEVKKFSVRDSSIPSPGCKEFNFYYEADSDATKPPNMENP	120		
DB	61	TKTIRRGARHRIHEVKKFSVRDSSIPSPGCKEFNFYYEADSDATKPPNMENP	120		
QY	121	WVKVDITIADESESOYDLGRVVKINTEVRSFGVRSRSGFYLAFOYGGCMSLIAVRVY	180		
DB	121	WVKVDITIADESESOYDLGRVVKINTEVRSFGVRSRSGFYLAFOYGGCMSLIAVRVY	180		
QY	181	RKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNDGELVPIGNC	240		
DB	181	RKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNDGELVPIGNC	240		
QY	241	MCKAGFEAVENGTVCRGCGSGTFKANOGEACTHCPINSRTTSEGATNCVRNGYRADL	300		
DB	241	MCKAGFEAVENGTVCRGCGSGTFKANOGEACTHCPINSRTTSEGATNCVRNGYRADL	300		
QY	301	DELDMCTTIPSAPOAVISSVNETSLMLETPPRDSGREDLVYNIKSCSGSGRACATR	360		
DB	301	DELDMCTTIPSAPOAVISSVNETSLMLETPPRDSGREDLVYNIKSCSGSGRACATR	360		
QY	361	CGDNVOYAPROGLTPRIYISDLAHTOYFEIAQVNVTOOSPPSPQFAVINTTQNA	420		
DB	361	CGDNVOYAPROGLTPRIYISDLAHTOYFEIAQVNVTOOSPPSPQFAVINTTQNA	420		

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Db 361 CGDNVOYAPROGLTEPRITISDLAHTQYFEIQAVNGVTDQSPSPQFASVNTTNOA 420
QY 421 APSAIVIMHOVSRTVSTILSMQSDPOPGVILIDYLOYTEKELSTYNAATKSPNTYT 480
Db 421 APSAIVIMHOVSRTVSTILSMQSDPOPGVILIDYLOYTEKELSTYNAATKSPNTYT 480
QY 481 GLKAGAIYVQVARTYAGRGYSKGMVFQTMTEAEYQTSIOEKLPLIIGSSAAGLVFLI 540
Db 481 GLKAGAIYVQVARTYAGRGYSKGMVFQTMTEAEYQTSIOEKLPLIIGSSAAGLVFLI 540
QY 541 AVVVAIYVCRNRRGEFADSEYTDKLOHYTSGHITPGMKIYIDPFYEDNEAVREAKEI 600
Db 541 AVVVAIYVCRNRRGEFADSEYTDKLOHYTSGHITPGMKIYIDPFYEDNEAVREAKEI 600
QY 601 DISCVATIEOYIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLEASIMGO 660
Db 601 DISCVATIEOYIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLEASIMGO 660
QY 661 FDRPNVITHLEGVYTKSTPVMIITEFMEGSLDSFLRQNDQFVIOVLGMKRGIAAGMKY 720
Db 661 FDRPNVITHLEGVYTKSTPVMIITEFMEGSLDSFLRQNDQFVIOVLGMKRGIAAGMKY 720
QY 721 LADMTNVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTYSALGKFPITRTAPE 780
Db 721 LADMTNVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTYSALGKFPITRTAPE 780
QY 781 AIQYRKFTSASDVWSYGIYVMEVWSYGERPYMTNODVINAIEODYRLPPMDCCSALH 840
Db 781 AIQYRKFTSASDVWSYGIYVMEVWSYGERPYMTNODVINAIEODYRLPPMDCCSALH 840
QY 841 QLMIDCQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIIPDYTSFN 900
Db 841 QLMIDCQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIIPDYTSFN 900
QY 901 TYDEWLEAIKMGOKESFANAGTSEYDVVSQMMEDILRVGYTLAHOXKILNSIQVMA 960
Db 901 TYDEWLEAIKMGOKESFANAGTSEYDVVSQMMEDILRVGYTLAHOXKILNSIQVMA 960
QY 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

RESULT 2
A56599
embryo kinase 5 - chicken
N:Alternate names: receptor tyrosine kinase Cck5
C:Species: Gallus gallus (chicken)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 04-Feb-2000
C:Accession: A56599
R:Pasquale, E.B.
Cell:Regulatory 2, 523-534, 1991
A:Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor
A:Reference number: A56599; MOID:92144672
A:Accession: A56599
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-995 <PAS>
A:Cross-references: GB:M62325; NID:g211448; PIDN:AAA48667.1; PID:g211449
A:Note: sequence extracted from NCBI backbone (NCBIN:81999, NCBI:P:82001)
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat R
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein K
F:628-896/Domain: protein kinase homology <KIN>
F:636-644/Region: protein kinase ATP-binding motif
F:919-985/Domain: SAM homology <SAM>

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Query Match 96.8%; Score 4950.5; DB 2: Length 995;
Best Local Similarity 95.6%; Pred. No. 4.2e-226;
Matches 930; Conservative 28; Mismatches 12; Indels 3; Gaps 2;
QY 1 LLAABETLMDSTTATVATLGMVHPPSGMEVSGYDENMNTIRTYQVCNVESSONMLR 60

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Db 23 LLAABETLMDSTTATVATLGMVHPPSGMEVSGYDENMNTIRTYQVCNVESSONMLR 82
QY 61 TFFIRRGARHRIHVEKESVRCOSSIPSPGCKEFENLYXEADEPDATKTFPMMEHP 120
Db 83 TTYIRRGARHRIHVEKESVRCOSSIPSPGCKEFENLYXEADEPDATKTFPMMEHP 142
QY 121 WVKVDITIADESESOYDLGGRVAKINTEVRSFGPVSRSRGFLAFODYGGCMLIAVRFY 180
Db 143 WVKVDITIADESESOYDLGGRVAKINTEVRSFGPVSRSRGFLAFODYGGCMLIAVRFY 202
QY 181 RRCPRITONGAIFQETFLCAESTSLVAANGSCITANAEEVDVPIKLYCNGDGMLVPIGR 240
Db 203 RRCPRITONGAIFQETFLCAESTSLVAANGSCITANAEEVDVPIKLYCNGDGMLVPIGR 262
QY 241 MCKAGFEAVENCTVCGCGSGTFKANOGEACTHOPINRSTSEGANVCNRYRADL 300
Db 263 MCKAGFEAVENCTVCGCGSGTFKANOGEACTHOPINRSTSEGANVCNRYRADL 322
QY 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGGREDLVYNILCKSCGSGGACTR 360
Db 323 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGGREDLVYNILCKSCGSGGACTR 382
QY 361 CGDNVOYAPROGLTEPRITISDLAHTQYFEIQAVNGVTDQSPSPQFASVNTTNOA 420
Db 383 CGDNVOYAPROGLTEPRITISDLAHTQYFEIQAVNGVTDQSPSPQFASVNTTNOA 442
QY 421 APSAIVIMHOVSRTVSTILSMQSDPOPGVILIDYLOYTEKELSTYNAATKSPNTYT 480
Db 443 APSAIVIMHOVSRTVSTILSMQSDPOPGVILIDYLOYTEKELSTYNAATKSPNTYT 502
QY 481 --GLKAGAIYVQVARTYAGRGYSKGMVFQTMTEAEYQTSIOEKLPLIIGSSAAGLV 538
Db 503 YQNLKAGITTYVQVARTYAGRGYSKGMVFQTMTEAEYQTSIOEKLPLIIGSSAAGLV 562
QY 539 LIAVVAIYVCRNRRGEFADSEYTDKLOHYTSGHITPGMKIYIDPFYEDNEAVREAKEI 597
Db 563 LIAVVAIYVCRNRRGEFADSEYTDKLOHYTSGHITPGMKIYIDPFYEDNEAVREAKEI 622
QY 598 KEIDISCVATIEOYIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLEASI 657
Db 623 KEIDISCVATIEOYIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLEASI 682
QY 658 MGOFDHPRNVITHLEGVYTKSTPVMIITEFMEGSLDSFLRQNDQFVIOVLGMKRGIAAG 717
Db 683 MGOFDHPRNVITHLEGVYTKSTPVMIITEFMEGSLDSFLRQNDQFVIOVLGMKRGIAAG 742
QY 718 MKTLADMTNVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTYSALGKFPITRTAPE 777
Db 743 MKTLADMTNVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTYSALGKFPITRTAPE 802
QY 778 APEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYMTNODVINAIEODYRLPPMDCCS 837
Db 803 APEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYMTNODVINAIEODYRLPPMDCCS 862
QY 838 ALHQMLDQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIIPDYT 897
Db 863 ALHQMLDQKORNRHPRFGQIVNTLDKMRNPNSLKAMAPLSSGINPLDRTIIPDYT 922
QY 898 SFNTVDWLEAIKMGOKESFANAGTSEYDVVSQMMEDILRVGYTLAHOXKILNSIQV 957
Db 923 SFNTVDWLEAIKMGOKESFANAGTSEYDVVSQMMEDILRVGYTLAHOXKILNSIQV 982
QY 958 MRAQNOIOSVEV 970
Db 983 MRAQNOIOSVEV 995

RESULT 3
A39753
protein-tyrosine kinase (EC 2.7.1.112) elk precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 04-Feb-2000

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C:Accession: A39753; S04327  
 R:Linotak, V.; Green, P.; Pawson, T.  
 M:Cell. Biol. 11, 2496-2502, 1991  
 A:Title: Characterization of elk, a brain-specific receptor tyrosine kinase.  
 A:Reference number: A39753; MUID:91203869  
 A:Accession: A39753  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-984 <LH0>  
 A:Cross-references: GB:M59814  
 R:Letwin, K.; Yee, S.P.; Pawson, T.  
 Oncogene 3, 621-627, 1988  
 A:Title: Novel protein-tyrosine kinase CDNA's related to fps/fes and eph cloned using anti-tyrosine kinase antibodies.  
 A:Reference number: S04327; MUID:94167102  
 A:Accession: S04327  
 A:Molecule type: mRNA  
 A:Residues: 605-984 <LET>  
 A:Cross-references: EMBL:X13411; NID:956094; PIDN:CAA31777.1; PID:956095  
 C:Gene: elk  
 A:Gene: elk  
 C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat  
 C:Keywords: Arg; autophosphorylation; kinase-related transforming protein; phosphoprotein  
 F:617-885/Domain: protein kinase ATP-homology <RIN>  
 F:625-633/Region: protein kinase ATP-binding motif  
 F:908-974/Domain: SAM homology <SAM>

Query Match	76.5%;	Score 3914.5;	DB 2;	Length 984;
Best Local Similarity	74.0%;	Pred. NO. 2.7e-177;		
Matches 717;	Conservative 128;	Mismatches 121;	Indels 3;	Gaps 2

Db	614	JDVSPKIEEYIGAGEFEYVKGRLLKPGKREIYVAIKTLKAGSEKORPDLSEASIMG	673
OY	660	QEDPHNVHLEGVYTKSPWMIITEPMENGSLDSFLRKNDQOFIVQLVGLRGIAGMK	719
Db	674	QEDPHNIIRLEGVYTKSPWMIITEPMENGALDSEFLRKNDQOFIVQLVGLRGIAGMK	733
OY	720	YLADNNVYHRLAARNILVNSNLVCKVSDFGLSRLEDDTSDPYTTSALGKFPJRMTPAP	779
Db	734	YLSEKNVYHRLAARNILVNSNLVCKVSDFGLSRLDQDTSDPYTTSALGKIPYRMTPAP	793
OY	780	EALQYRKFTSASDVNSYSGIVMVEVMSYGERPYWMDTNDQVINALIEODYRLRPPMDCPSAL	839
Db	794	EALAKRKFTSASDVNSYSGIVMVEVMSYGERPYWMDSNDQVINALIEODYRLRPPMDCPSAL	853
OY	840	HQLMLDCQOKDRNHRPKFGQIVNTLDKMIIRNPNSIKAPALSSGILNPLDLRTDPTDYTSF	899
Db	854	HQLMLDCQOKDRNHRPKFGQIVNTLDKMIIRNPASIKTAVTAVAPSOPLDPTDYTSF	913
OY	900	NTVDWMLEAIKMGQKKESEFANAAGFTSPDVNSQMMMEDILRQGVYTLAGHOKKILINSIQYMR	959
Db	914	TTVDWMLEAIKMGQKKESEFANAAGFTSPDLQVQMTSEDLIRIGVYTLAGHOKKILINSIQYMR	973
OY	960	AQMNQIOQSV 968	
Db	974	QVMNQSPSV 982	

## RESULT 4

1516/2  
receptor tyrosine kinase - African clawed frog

C:Species: xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 18-Jun-1999  
C:Accession: F51573

C. Accession: 1310/2  
R. Jones, T. L.; Karavanova, I.; Maeno, M.; Ong, R. C.; Kung, H. F.; Daar, I. O.  
Oncogene 10: 1111-1117, 1995

A:Title: Expression of an amphibian homolog of the Eph family of receptor tyrosine kinases  
A:Reference number: 151672; MUID:95215070

A:Accession: I51672  
A:Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA  
A: Residues: 1-985 <JON>

A:Cross-references: EMBL:U4164; NID:g95/214; PIDN:AAV4888.1; PID:g95/215  
C:Genetics:  
J:Case: YNR

A:gene: AEN  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: AMP; transmembrane protein

GeneFmols: htf, transmembrane protein  
F:618-886/Domain: protein kinase homology <KIN>  
F:626-634/Region: protein kinase ATP-binding motif

F:909-975/Domain: SAM homology <SAM>

Query Match	73.48	Score 3754	DB 2	Length 985
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Best Local Similarity 71.6%; Pred. NO. 9./e-10;  
Matches 693; Conservative 131; Mismatches 134; Indels 10; Gaps 5;

2 LAAVEETLMDSTTATAELGMVHPSPGMEEYSGYDENMNTIRTYQVCNVESSONMRLRT 61

Db 17 VGAVEETLMDTRATAEIGWTFANPSSGMEEYSGYDENLNTIRTYQVCNVGPKQNNMLLT 76

[illegible]

Db 77 TFI PRG A H R Y V E M R T V R D C S S L P H V P G S C K E T F N L Y I E T D S I E N K I S T F M N E S P Y 136

[illegible]

00 182 KCDPTONGCAIHOETISGAESMSTIVABRGSCITANAEVUDVPTIKVINGNGDHWIYDPTGRCM 241

197 EMSWYNLLTPVPEETMGAEESLSLTARGTCLPNAEEVDVILKLCNGDGEHMPVIGKCT 256

242 CKAGFEAVENGTVCRGCPGCTFKANOGDEACTHCPINSRTTSEGATNCVCBNGYYRADLD 301

[illegible]

Db 257 CKAGEBP-ENHVVCKACPAAMFRKANOGMIGIACCPANRSTSEASPICICRNGCYRADFD 315  
 QY 302 PLDMPTTIPSAQAVISSVNETSIMLEMTPPRDSGREDLVNITICKSGSGRGACTRC 361  
 Db 316 TPAPCTSVSGRNVIISTVNETAITLEMHPPRETGGRDVDVNIYCKCRADRACSRG 375  
 QY 362 GDNVQYAPRQLGTEPRITYSIDLATQYFEIQAQVGVDDSPFSQFASVITITNOAA 421  
 Db 376 DDNVVDPRQLGLDTRVFLISNMAHTPYFEIQAQVNGVYTKNSPFPQHVSVITITNOAA 435  
 QY 422 PSASVIMHOVSRTVDSITLWSQPDOPNGVILDELYQYKEKELSEYNAFAIKSPNTV-- 479  
 Db 436 PSSVPIMHOVKATMKISITLWSQPDOPNGIILDEYIRYEEKHEHFNSSILARSQNTARR 495  
 QY 480 TGKAKAIVYE--OYRARVAGYGRYSGKMYQMTLEAYQTSIOEKLPLIIGSSAAGL 536  
 Db 496 TG--GRVMFMSSVQYRARKVAGYKGFSSQGFOTLAEYKSELREQLPL-TGSAAGV 551  
 QY 537 VFLLAVVIAIVCNRRGFERADSEYTDKLOHYTSGHITFGMKIYIDPFTYEDPNEAVREF 596  
 Db 552 VFIVSLVIAISVCSRRKRTYSKEAVYSDKLOHYSTGRSGROMKIYIDPFTYEDPNEAVREF 611  
 QY 597 AKETIDISVAKIEOYIAGERGEVCSGHLKPGKREIYFAIKTKLSGYTERKORDFLSEAS 656  
 Db 612 AKEDIVSFYKIEEVIAGERGEVYKGRKLPSKREISVAIKTKLAGYSEKORDFLSEAS 671  
 QY 657 IMQGFHPNVIHEGVYVSTPYMITTEPMENGLSDSLRONGQOTVYQVLMGLGIAA 716  
 Db 672 IMQGFHPNVIHEGVYVSTPYMITTEPMENGLSDSLRONGQOTVYQVLMGLGIAA 731  
 QY 717 GMKYLADMYVHRDLAARNILVNSNLVCKVSDGSLRFLSDPTYSALGKPEPIRM 776  
 Db 732 GMKYLSEMYVHRDLAARNILVNSNLVCKVSDGSLRFLSDPTYSALGKPEPIRM 791  
 QY 777 TAPAEIQYKRTSASDVWSYGIYMEVMSYGERPYWMTNODVINAIEDYRLPPMDCP 836  
 Db 792 TQOEALYARKFTSASDVWSYGIYMEVMSYGERPYWMTNODVINAIEDYRLPPMDCP 851  
 QY 837 SALHOLMLCQWOKDRHRKFGQIVNTLDKIRNPNSLAKMAPLSSGIMPLIDRTIPY 896  
 Db 852 ALHOLMLCQWOKDRHRKFGQIVNTLDKIRNPNSLAKMAPLSSGIMPLIDRTIPY 911  
 QY 897 TSEFTVDEMLEAIKMGQYKESFANAGFTSDVVSQMMEDILRVGYTLAGHOKILINSIO 956  
 Db 912 SAFTSVDMLSAIKMGQYKDNFLSGFTSLQYVAQWTSDDLRTIGTLAGHOKILINSIO 971  
 QY 957 VMRAQMNQ 964  
 Db 972 SMKVOITQ 979  
 RESULT 5  
 150612  
 protein-tyrosine kinase (EC 2.7.1.112) Cdk6 - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 04-Feb-2000  
 C:Accession: I50612; S33503  
 R:Sajjadi, F.G.; Pasquale, E.B.  
 Oncogene 8, 1807-1813, 1993  
 A:Title: Five novel v-src-related tyrosine kinases are differentially expressed.  
 A:Reference number: I50611; MUID:93288394  
 A:Accession: I50612  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-952 <SAJ>  
 A:Cross-references: EMBL:Z19110; NID:G312901; PIDN:CAA79526.1; PID:G312902  
 C:Genetics:  
 A:Gene: Cdk6  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: Arp; phosphotransferase; transmembrane protein; tyrosine-specific protein k  
 F:585-853/Domain: protein kinase homology <KIN>  
 F:593-601/Region: protein kinase Arp-binding motif  
 F:876-942/Domain: SAM homology <SAM>

Query Match 72.5%; Score 3707; DB 2; Length 952;  
 Best Local Similarity 70.2%; Pred. No. 1.5e-167;  
 Matches 687; Conservative 120; Mismatches 118; Indels 54; Gaps 4;  
 QY 7 ETLMDSTTAAELGAMVHVPSSGMEVSYGDEMNNTIRYQVCVFPSSONNMILRTFIRR 66  
 Db 1 ETLMDRTATAEIGMTANPSPSGMEVSYGDEMNNTIRYQVCVFPSSONNMILRTFIRR 60  
 QY 67 RGAHRIYHEKESVHDCSSIPSVGSKCTEFNLVYEADFDSATKTFPMMENPVKYVD 126  
 Db 61 RGAHRIYHEKESVHDCSSIPSVGSKCTEFNLVYEADFDSATKTFPMMENPVKYVD 120  
 QY 127 IAADEFQYVDLGGRYMKTINTEVRSFVPSRSGFYLAPODYGGCSLIAVRFYRKCPPI 186  
 Db 121 IAADEFQYVDLGGRYMKTINTEVRSFVPSRSGFYLAPODYGGCSLIAVRFYRKCPPI 148  
 QY 187 IONGALFOETLSGAEISTVLAARGSCIANAEYDVPITKLYCNGDGEMLVPIGRCKKAGF 246  
 Db 149 VONFAIFPETMTGAEISTVLAARGSCIANAEYDVPITKLYCNGDGEMLVPIGRCKKAGF 208  
 QY 247 EAVNGTVCRGCPSTCFKANOGDEACTHCPINSRTSEGATNCVCNNGRYRADLPLDMP 306  
 Db 209 EP-ENNVACRACPACTCFKANOGDEACTHCPINSRTSEGATNCVCNNGRYRADLPLDMP 267  
 QY 307 CTITPSAPQAVISSVNETSIMLEMTPPRDSGREDLVNITICKSGSGRGACTRCGDNVQ 366  
 Db 268 CTITPSAPQAVISSVNETSIMLEMTPPRDSGREDLVNITICKSGSGRGACTRCGDNVQ 327  
 QY 367 YAPRQLGTEPRITYSIDLATQYFEIQAQVGVDDSPFSQFASVITITNOAAPSAS 426  
 Db 328 YAPRQLGTEPRITYSIDLATQYFEIQAQVGVDDSPFSQFASVITITNOAAPSAS 387  
 QY 427 IMHOVSRTVDSITLWSQPDOPNGVILDELYQYKEKELSEYNAFAIKSPNTV-- 467  
 Db 388 IMHOVSRTVDSITLWSQPDOPNGVILDELYQYKEKELSEYNAFAIKSPNTV-- 447  
 QY 468 NATAIKSPNTV--VIGLKGALVYQVARKYAGYGRYSGKMYQMTLEAYQTSIOEKL 525  
 Db 448 NATAIKSPNTV--VIGLKGALVYQVARKYAGYGRYSGKMYQMTLEAYQTSIOEKL 507  
 QY 526 PLIGSSAGIYFLAVVIAIVCNRRGFERADSEYTDKLOHYTSGHITFGMKIYIDPFT 585  
 Db 508 PLIGSSAGIYFLAVVIAIVCNRRGFERADSEYTDKLOHYTSGHITFGMKIYIDPFT 567  
 QY 586 YEDPNEAVREFAKEIDISCVKIEOYIAGERGEVCSGHLKPGKREIYFAIKTKLSGYTE 645  
 Db 568 YEDPNEAVREFAKEIDISCVKIEOYIAGERGEVCSGHLKPGKREIYFAIKTKLSGYTE 627  
 QY 646 KORRDFLSEASTMGQFDHNPVTHLGVYTKSPVMITTEPMENGLSDSLRONGQOTVY 705  
 Db 628 KORRDFLSEASTMGQFDHNPVTHLGVYTKSPVMITTEPMENGLSDSLRONGQOTVY 687  
 QY 706 QLVGMRLGIAAGMKYLAADMYVHRDLAARNILVNSNLVCKVSDGSLRFLSDPTYS 765  
 Db 688 QLVGMRLGIAAGMKYLAADMYVHRDLAARNILVNSNLVCKVSDGSLRFLSDPTYS 747  
 QY 766 SALGKFPRTKWTAPARAIOYKRTSASDVWSYGIYMEVMSYGERPYWMTNODVINAIED 825  
 Db 748 SALGKFPRTKWTAPARAIOYKRTSASDVWSYGIYMEVMSYGERPYWMTNODVINAIED 807  
 QY 826 DYRLPPMDCPSALHOLMLCQWOKDRHRKFGQIVNTLDKIRNPNSLAKMAPLSSGIN 885  
 Db 808 DYRLPPMDCPSALHOLMLCQWOKDRHRKFGQIVNTLDKIRNPNSLAKMAPLSSGIN 867  
 QY 886 IPLDRTIPDYTSFNTVDEMLEAIKMGQYKESFANAGFTSDVVSQMMEDILRVGYTLA 945  
 Db 868 IPLDRTIPDYTSFNTVDEMLEAIKMGQYKESFANAGFTSDVVSQMMEDILRVGYTLA 927  
 QY 946 GHOKKIINSIOVMRAQMNQ 964  
 Db 928 GHOKKIINSIOVMRAQMNQ 946





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Db 333 DSACTTTPSPRPVIAVNTSTILKMSERDQVGRDLDLITVCKCKHAGASACSRK 392
QY 362 GDNVQAPAROLGLTEPRITYISDLAHTQYTFEIQAVNGVTDOSFPSPQASVNTTNOAA 421
Db 393 DDVVEFPRLGLSEPRVHTSHLAHRTYTFEVOAVNGVSGKSPLPRAVAVNTTNOAA 452
QY 422 PSATVIMHGVSRFVDSITLMSQPDQPNGVITLDELYQYKEKSEYNATIKSPNTV-- 479
Db 453 PSEVPTLRLHSSGSLTSLMAPPENGVILDEYEMKTEFK--SEGLASVTSQMSVOL 510
QY 480 TGLKAGIIVFOYRARTVAGYGRGMYFQMTF-AEYQTSIOEKLPLITIGSSAALVF 538
Db 511 DGLRPAPRVYVYRARTVAGYGRGMYFQMTF--SEGLASVTSQMSVOL 570
QY 539 LIAVVAIVAIYCNRRGERADSEYTDKLOHTYSGHITPGMKIYIDPPTYEDPNAVEFAK 598
Db 571 VVAVVAIVAIYCNRRGERADSEYTDKLOHTYSGHITPGMKIYIDPPTYEDPNAVEFAK 626
QY 599 EIDISCVKIEOVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEASIM 658
Db 627 EIDVSCVKIEVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEASIM 686
QY 659 GQPDHNVITLHLEGVYTKSTPVMITTEPMENGSLDSEFLRONDQGFYIOLVGLRGIAAG 718
Db 687 GQPDHNVITLHLEGVYTKSTPVMITTEPMENGSLDSEFLRONDQGFYIOLVGLRGIAAG 746
QY 719 KYLADNNVYHRLAARNLIVNSLVCKVSDFGLSRLEDDTSPTYSALGKFPRLMWA 778
Db 747 KYLSENNVYHRLAARNLIVNSLVCKVSDFGLSRLEDDTSPTYSALGKFPRLMWA 806
QY 779 PEAIQYRKFTSADVWSYGIYVMEVWSYGERPYWDMTNDVINAIBODYRLPPMCPSPA 838
Db 807 PEAIARKFTSADVWSYGIYVMEVWSYGERPYWDMTNDVINAIBODYRLPPMCPSPA 866
QY 839 LHLQMLDCKQKRNHRPRKGOIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPDYS 898
Db 867 LHLQMLDCKQKRNHRPRKGOIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPDYS 926
QY 899 FNTVDEMLEAIKMGQYKESFANAGFTSPDYVSGMMEDILRGVITAGHOKTILNSIQM 958
Db 927 FNTVDEMLEAIKMGQYKESFANAGFTSPDYVSGMMEDILRGVITAGHOKTILNSIQM 986
QY 959 RAQMNOIOSVEV 970
Db 987 RLQMNQTLFVQV 998

RESULT 8
148653
mouse developmental kinase 5 (MDK5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: 148653
R:Clousek, T.; Lerch, M.M.; Ullrich, A.
Oncogene 11, 2085-2095, 1995
A:Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two nc
A:Reference number: 148652; MUID:96074837
A:Accession: 148653
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-993 <RES>
A:Cross-references: EMBL:249086; NID:q1089899; PIRN:CAA8910.1; PID:q1089900
C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat
C:Keywords: ATP; transmembrane protein
F:626-894/Domain: protein kinase homology <KIN>
F:634-642/Region: protein kinase ATP-binding motif
F:917-983/Domain: SAM homology <SAM>

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Query Match 70.4%; Score 3604; DB 2; Length 993;  
 Best Local Similarity 70.1%; Pred. No. 1,le-162;  
 Matches 683; Conservative 111; Mismatches 163; Indels 18; Gaps 6;

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QY 4 AVEETIMDSTTATAEIGMAYHPSPSGWEVSGYDENNTTITRTVOYCNVESSQNMWLRIKF 63
Db 29 ALRETTIMDCKWVYSELAMTSHPESSGWEVSGYDEANMPITRTVOYCNVRESSQNMWLRTGF 88
QY 64 IRRGARIHIVEKKFVRCOSSIPVPGSCKEFENLYYEAQDSDSTKTFPMNEMPMWK 123
Db 89 IRRVQRYVILKFTVRDONSIPNIPGSCKEFENLYYEAQDSDSTKTFPMNEMPMWK 148
QY 124 VDTIADESFQYDLGGRYMKITTEVRSFPGVSRSGFYLAFOYGGCKMLIAVRYFRKC 183
Db 149 VDTIADDESRLDAG---RVNTKYRSPGLSKAGFYLAFOYGGCKMLISVIRAGDKKC 204
QY 184 PRITQNGALFOETLSAESTSLVAANGSCILANAEVDVYIKLYCNGDGWLVPIGRCKC 243
Db 205 ASTTAGAFALPETLNGAEPSTSLVAPGTCILANAEVSVPLKLYCNGDGWLVPIGRCKC 264
QY 244 AGFEAVENGTCVCGPSGFGFKANQGDGECTHCPINRRTSEGATNCVRNGYRADLPL 303
Db 265 TGEHPAKESQCRACPGSYKAKQGGPCLPCPPNRTTSPASICTCHANNFYRADSDSA 324
QY 304 DMECTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVNITCKSCSGGGA----C 358
Db 325 DSACTTEPSPRPVIAVNTSTILKMSERDQVGRDLDLITVCKCKHAGASACSRK 384
QY 359 TTRGDNVQAPAROLGLTEPRITYISDLAHTQYTFEIQAVNGVTDOSFPSPQASVNTT 418
Db 385 SRQDNVVEFPRLGLSEPRVHTSHLAHRTYTFEVOAVNGVSGKSPLPRAVAVNTT 444
QY 419 QAPASVSIHMOVSRFVDSITLMSQPDQPNGVITLDELYQYKEKSEYNATIKSPNT 478
Db 445 QAPASVPTLRLHSSGSLTSLMAPPENGVILDEYEMKTEFK--SKIASTVYSQMS 502
QY 479 V--TGLKAGIIVFOYRARTVAGYGRGMYFQMTF-AEYQTSIOEKLPLITIGSSAAG 535
Db 503 VQDGLQPDAPRVYVYRARTVAGYGRGMYFQMTF--SEGLASVTSQMSVOL 562
QY 536 LVELLAVVAIVAIYCNRRGERADSEYTDKLOHTYSGHITPGMKIYIDPPTYEDPNAVE 595
Db 563 FEFMAVVAIVAIYCNRRGERADSEYTDKLOHTYSGHITPGMKIYIDPPTYEDPNAVE 618
QY 596 FAKEDIDSCVKTIEOVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEA 655
Db 619 FAKEDIDSCVKTIEOVITGAGEFEGVSGHILKLPGRKEIFVAIKTKSGYTEKORRDLSEA 678
QY 656 SIMGQPDHNVITLHLEGVYTKSTPVMITTEPMENGSLDSEFLRONDQGFYIOLVGLRGIA 715
Db 679 SIMGQPDHNVITLHLEGVYTKSTPVMITTEPMENGSLDSEFLRONDQGFYIOLVGLRGIA 738
QY 716 AGMKYIADNNVYHRLAARNLIVNSLVCKVSDFGLSRLEDDTSPTYSALGKFPRL 775
Db 739 AGMKYIADNNVYHRLAARNLIVNSLVCKVSDFGLSRLEDDTSPTYSALGKFPRL 798
QY 776 WTAPAIQYRKFTSADVWSYGIYVMEVWSYGERPYWDMTNDVINAIBODYRLPPMDC 835
Db 799 WTAPAIARKFTSADVWSYGIYVMEVWSYGERPYWDMTNDVINAIBODYRLPPMDC 858
QY 836 PALHQLMLDCKQKRNHRPRKGOIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPD 895
Db 859 PALHQLMLDCKQKRNHRPRKGOIVNTLDKMTIRNPNSIKAMAPLSSGINLPDLRTIPD 918
QY 896 YTSFNTVDEMLEAIKMGQYKESFANAGFTSPDYVSGMMEDILRGVITAGHOKTILNSI 955
Db 919 YTSFNTVDEMLEAIKMGQYKESFANAGFTSPDYVSGMMEDILRGVITAGHOKTILNSI 978
QY 956 QVRAQMNOIOSVEV 970
Db 979 QDMRLQMNQTLFVQV 993

RESULT 9
149071
protein kinase - mouse (fragment)

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A:Molecule type: mRNA  
 A:Residues: 1-991 <RES>  
 A:Cross-references: GB:U36644; NID:9551611; PIDN:AAA74245.1; PID:9551612  
 C:Genetics: HEK7  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 F:627-893/Domain: protein kinase homology <kin>  
 F:916-982/Domain: SAM homology <SAM>

Query Match 59.2%; Score 3031; DB 2; Length 991;  
 Best Local Similarity 59.1%; Pred. No. 1,9e-135;  
 Matches 567; Conservative 163; Mismatches 216; Indels 14; Gaps 10;

6 EETLMDSTTATAEIGMWHPPSGMEVSGYDENNTIRTYQVCNVFESSONNMLRTKFR 65  
 36 EVNLDSRTVWGDLGMIAPKNGWEEIGEVDENYAPIHTYQVCNVFESSONNMLRTKFR 95  
 66 RRGARHRIHVEKKEFVRCSSIPSPGSCKEFNLYYEADPDSATKTFPPMMENPMYKVD 125  
 96 NEGSRRIEIKFTLRCCNSLPGLGTCCKETFFNNYFESDQNGR---NIKEQYIKID 151  
 126 TIADESFSDVDLGRVMTKITEVRSRSGFYLAPODYGCMGLIARVFEYRCPR 185  
 152 TIADESFTELDDRMKLTETEDVNDVPLSKGFTLAFQVGCIALVSRVYTKKCP 211  
 186 IONGAIFOETLSGAESTSLVAARSGCIANAEEVDPIKLYCNGDEMLVPIGRCKAG 245  
 212 VVRLHAFVPTITGADSSQLLEVSGSCV-NH5VDEPPKMKSHGEMVLPIGCKMCKAG 270  
 246 FEAVENTVRCGCGSGTFKANGODEACTHCPINSRTTSEGATNCVCNRYRADLDPLDM 305  
 271 YEE-KNCT-QVCNPGPFKASPHLQSGCKCPHSTYTHEASTVSCVCKDFRRESDDPTM 328  
 306 PCTTIPAPDAVISVNETSLMLEMPPRDGGREDLVYNIICKSGSGGACTRCGDV 365  
 329 ACTPAPAPNAISNVETSEVLEMPRPADTGKADVIYIACKCKSHAGVCECGGHV 388  
 366 QYARQLGLTEPRITYSIDLAAHTQYFEIOAVNGVTQDSPSPFOPASVNTTNOAPSAY 425  
 389 RYLPKROGLKNTSYMMVMDLAAHTNYFEIADVNGVSDLSGARGVSVNTTNOAPSAY 448  
 426 SIMNOVSRTVDSITLSMSQDOPRGVILDELOYEKELESEYNAITAKSPNTYT--GLK 483  
 449 TNWKKGIANKNSISLSQEDPRPGIILEYKIHFKEND-OETSYTIKSKETITTAGLK 507  
 484 AGAIYVQVARTVAGYGRYSCKMYFQMTAEAYOTSIQKELPLIGSSAAGFLIAYV 543  
 508 PASVYVQIARITAGYGVSRREFET-TPVFAASDQSIPIYANSVTVGVILLAVI 566  
 544 VIALVCRKGFERRADSEYTDKLQHTYSGHT-TPGMKIYIDPFTYEDPNEAVREFAKEDI 602  
 567 GVLISGRRCYSKAKODPEEEKMHFHNGHIKLPGRVITYIDPHYTEDPNQAVHEFAKIEA 626  
 603 SCVIEBOVITAGEGEVCSGLKLPGRKREIFVAILTKLSQYTEKQORDFSEASIMQED 662  
 627 SCITIEVITAGEGEVCSGLKLPGRKREIFVAILTKLSQYTEKQORDFSEASIMQED 666  
 663 HPNVIHLEGVYVTKSTPYMITTEFMENGLSDFLRONDQFTYIQLVGLMGLIAGMKYLA 722  
 687 HPNVIHLEGVYVTKSTPYMITTEFMENGLSDFLRONDQFTYIQLVGLMGLIAGMKYLA 746  
 723 DMNIVHDLAARILNLSNLYCVSDFGSLRLEDDTSDFTYVSALGKFPFIMTAPAEI 782  
 747 DMNIVHDLAARILNLSNLYCVSDFGSLRLEDDTSDFTYVSALGKFPFIMTAPAEI 804  
 783 QYKRTFSASQVMSYGIYMEVMSYGERPYMDMTNODVYINIEDDYRLPPMDPSALHOL 842  
 805 AFKRTFSASQVMSYGIYMEVMSYGERPYMDMTNODVYINIEDDYRLPPMDPSALHOL 864  
 843 MLDCKMDRHHRRKFGQIVNTLDKMIKRNPSLAKAMAPLSSGINKPLDRTIPDYTSNTV 902  
 865 MLDCKMDRHHRRKFGQIVNTLDKMIKRNPSLAKAMAPLSSGINKPLDRTIPDYTSNTV 924

QY 903 DEWLEAIKMGQYKESFANAGTFSDVYSQMMEDILRVGVTLAGHOKKILNSIQVNRQM 962  
 DB 925 GEMLEAIKMGRTYEIFEMENGYSSMDVAQVTLDELRLGLVTLVGHOKKINSIQEMKVL 984

## RESULT 13

protein-tyrosine kinase (EC 2.7.1.12) Eph precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Nov-1997 #sequence, revision 05-Dec-1997 #text, change 04-Feb-2000

C:Accession: S78059; S30505; I58366

R:Charnay, P.  
 submitted to the EMBL Data Library, March 1992

A:Reference number: S78059

A:Accession: S78059

A:Molecule type: mRNA

A:Residues: 1-986 <CHAS>

A:Cross-references: EMBL:X65138; NID:954083; PIDN:CAA46268.1; PID:954084

R:Gillardi-Hebensreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chester, A.; Wilkin  
 Oncogene 7, 2499-2506, 1992

A:Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed 1

A:Reference number: S30496; MUID:93096484

A:Accession: S30505

A:Molecule type: mRNA

A:Residues: 1-31,55-986 <GIL>

A:Cross-references: EMBL:X65138

C:Genetics: Sek

C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat

C:Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase

F:1-15/Domain: signal sequence #status predicted <Sig>

F:16-986/Product: protein-tyrosine kinase Eph #status predicted <NMT>

F:548-569/Domain: transmembrane #status predicted <TM>

F:619-885/Domain: protein kinase homology <kin>

F:627-635/Region: protein kinase ATP-binding motif

F:908-974/Domain: SAM homology <SAM>

F:235,340,408,423/Binding site: carboxyrate (Asn) (covalent) #status predicted

Query Match 59.1%; Score 3026; DB 2; Length 986;  
 Best Local Similarity 59.3%; Pred. No. 1,9e-135;  
 Matches 580; Conservative 144; Mismatches 212; Indels 42; Gaps 14;

4 AVEETLMDSTTATAEIGMWHPPSGMEVSGYDENNTIRTYQVCNVFESSONNMLRTKFR 62  
 DB 28 ANEVTLLDSNSVQELGIMWISPLEGMEBSINDEXPTIRTYQVCNVFESSONNMLRTKFR 87  
 QY 63 FIRRGAHRIHVEKKEFVRCSSIPSPGSCKEFNLYYEADPDSATKTFPPMMENPMYKVD 122  
 DB 88 WITREGAORVYIEIKFTLRCCNSLPGLGTCCKETFFNNYFESDQNGR---NIKEQYIKID 143  
 QY 123 KVTPIADESFSDVDLGRVMTKITEVRSRSGFYLAPODYGCMGLIARVFEYRCPR 182  
 DB 144 KVTPIADESFTELDDRMKLTETEDVNDVPLSKGFTLAFQVGCIALVSRVYTKKCP 203  
 QY 183 HPNVIHLEGVYVTKSTPYMITTEFMENGLSDFLRONDQFTYIQLVGLMGLIAGMKYLA 242  
 DB 204 CPLTVNRNLQFPDITIGADTSLVYRSGCVNNSEKDV-KMYCGADGEMVLPIGCKMCKAG 262  
 QY 243 KAFPEAVENGTVCRCGSGTFKANGODEACTHCPINSRTTSEGATNCVCNRYRADLDPLDM 302  
 DB 263 NAGHEE-QNGE-CQACKIGYKALSTDASCACPKPSYVMEGATCTCDRGFFRADNDNA 320  
 QY 303 LDPKCTTIPAPDAVISVNETSLMLEMPPRDGGREDLVYNIICKSGSG-NGACTRC 361  
 DB 321 ASNPCTRPSPAPLNLISNVNETSVNLEFMSPOVTGGRQDSTVNVCKKCGAGPSKCRPC 380  
 QY 362 GDNVQYARQLGLTEPRITYSIDLAAHTQYFEIOAVNGVTQDSPSPFOPASVNTTNOAPSAY 421  
 DB 381 GSGVHTYPOONGIKTTRVSTITDLAAHTNYFEIADVNGVSDLSGARGVSVNTTNOAPSAY 440  
 QY 422 PSANVSIHQVSRIVDSITLSMSQDOPRGVILDELOYEKELESEYNAITAKSPNTYT--GLK 479

Db 441 PSSIALVQAKEVTRYVALWMLPEDRPENGVLTEEVKTYEKEDQNRSTRIVYIARNTDI 500  
 Oy 480 TGLNAGAIYVEQVRAFYAGYGRYSGKMYFQTMTEAEQTSIOEKLPLTIGS----- 531  
 Db 501 KGLNRLTGYVEHVARRTAAGYGDSEPLEYVTTNT-----VPSRIIGDGNSTVL 549  
 Oy 532 --SAAQVFLIAVVVIAIVCNRR--GFERADSEYTDKLTQHTSGHITPGMKIYIDPEFYE 587  
 Db 550 LVSVSGSVLVVLLVIAIAVVISRRRSKYAKQAEDE-----KILNAGVTVYADPEFY 603  
 Oy 588 DPNEAVREFAKEIDISCYKIEOVIGAGEFGEVCSGHLKLPGRREIFVAIKTLKSGYTEKQ 647  
 Db 604 DPNQAVREFAKEIDASCIKIEKIVIGGEFGEVCSGRLKVPGRREICVAIKTLKAGYTDKQ 663  
 Oy 648 RRDFTSEASIMGQEDHPNVVILHEGVYKSTPVMITTEEMENGSIDSFRLQNDGQFTVIQL 707  
 Db 664 RRDFTSEASIMGQEDHPNVIHLEGVYTKSTPVMITTEEMENGSIDSFRLQNDGQFTVIQL 723  
 Oy 708 VGMNLGIAAGKMYTADNMVYVRHDLAARNILVNSNYCVKVSDFGSRFLPDDTSDPTYSYA 767  
 Db 724 VGMNLGIGSGMYTSDMSYVHRDLAARNILVNSNYCVKVSDFGSRFLPDDTSDPTYSYA 782  
 Oy 768 LGGKPEIPMTAPPEALQYRKFTSASDVSYGIVMVEVMSYGERPYWDMTNODVINAIEDQY 827  
 Db 783 -GGKIPIMTAPPEALQYRKFTSASDVSYGIVMVEVMSYGERPYWDMTNODVINAIEDQY 841  
 Oy 828 RLPPMDCPSALHQLMDLQWQKDRNRHRRKFGQIVYTLTKMIRNPMSLAAAPLSSGILNP 887  
 Db 842 RLPPMDCPSALHQLMDLQWQKERSDRKFGQIVYTLTKMIRNPMSLKRGSSESRPMTA 901  
 Oy 888 LLDRTIPDYTSFNVDENWLEAIKMGQYKESFANAGFTSFVDVSCQMMMDIIRVGTTLA 947  
 Db 902 LLDPSPEFSANVSGVMDLQAKMDRYKDNFTNAGYITLLEAVVHMSQDDLARIGITALTH 961  
 Oy 948 OKILNLSIQVMRAQMNQI 965  
 Db 962 OKILNLSIQVMRAQMNQI 979

RESULT 14  
 158351  
 receptor protein-tyrosine kinase - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
 C:Accession: 158351  
 C:RefSeq: H01st, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995  
 A>Title: cDNA Cloning and tissue distribution of five human EPH-like receptor protein-tyr  
 A:Reference number: 158351; MUID:95206782  
 A:Accession: 158351  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-998 <RES>  
 A:Cross-references: GB:L36642; NID:g551607; PIDN:AAA74243.1; PID:g551608  
 C:Genetics:  
 A:Gene: HEK11  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
 F:631-897/Domain: protein kinase homology <KIN>  
 F:633-647/Region: ATP-binding motif  
 F:920-986/Domain: SAM homology <SAM>

Query Match	59.0%;	Score 3016;	DB 2;	Length 998;
Best Local Similarity	59.1%;	Pred. No. 5.7e-135;		
Matches 574;	Conservative 151;	Mismatches 224;	Indels 22;	Gaps 10

0y 3 AAVENTLMDSTTAAALGCMWYHPPSGMEVNSCYDENMNTITPTVCYAVFESSQNNMLRTK 62  
||| |::| ||| :|::|::|::| ||| ||||||| |::|::|  
Db 29 AAKEYLLDLSKAQOTEELEMISSPENGMBEISGLDEENTPIRTIYQCVMEPNQNMLRLTN 88  
  
0y 63 FIRRRGAHRIVEAKFSYRDCSSIPSYPGSKETFFNLITYEAEDSDATKTIFPMNMENPW 122

Db	89	WISGNAQRIFVELKATLRLRONSPLGVLTGCKTFMUYIYYEDYD---TGNINENLYV	144
Qy	123	KVDYITAADESEFOYDGLGRVYKINTEVERSEFPVSRSGFYLAFOYDGGCMLIAVREYRK	182
Db	145	KIDYITADESEPTQDGLGERMKKINTEVERIGLPSKRGFYLAFOYDAGACIALVSVREYRK	204
Qy	183	CPRIIONGAIQFOEFLSGAESTSYAARGSIANA-EVDVPIKLIIONGDEMLVPIGCM	241
Db	205	CWSTIENTIALEPDIYVITSESSLVERGTVSSAEEAENAPRMHCASAGEMLVPIGCI	264
Qy	242	CKAGEAVENTGVCJPGSGTFRKANOGDEACTCPIINSTRTSEGATNCVRNMYRADLD	301
Db	265	CKAGYO-QKGDICEQGGRGFYKSSSQDQCCNSCPIHSPDSKDESRCEDEGYRABSD	322
Qy	302	PLDMCPTTISAPQAVISSYNETSLIMEWTPPRDSGSGREDLYNINITCKSCSGGRACIRC	361
Db	333	PPYVACTRPPSAPONLJFNINQTTVSLSEMSPPADNGRNDYRILICKCSWEQECVPC	382
Qy	362	GDNQVAPRQGLREPRITSLIDLAHQYFFELQVANOAGTQDSPESPAPASVINITNOAA	421
Db	383	GSNIGYAPQDGLGENDYVMDLHAHANTFYFEVBAVNGSDLSRSQRLEFANSTITGGAA	442
Qy	422	PSAVSIMHQSRTVDJITLSMSPQDPOENGVIIDYELQYIEKELSE-YANATAKSEPTVY	479
Db	443	PSQSVGVKREKVLQRSVELSMOEPENHNGITFEYIEKYEKQDREKTYSTVTKSTASAI	502
Qy	480	TGLKAGAIYVQVAPRVAVCYGRSGCMYQWTEA----EYQTSIOKJLPLIGS--S	532
Db	503	NNLKPRTYVYQIAFAFPAAGISNPSLDVATLEETATGMFEFVAVSSQONPVIIIAVYA	562
Qy	533	AAGLVFLAAVVVIAIVONRR-GEFRADSEYTDKLOHYTSGHITPGKRIIDPFTYEDNE	591
Db	563	VAGTILIVFMVFGTIGRRHOGYSKADQDEDELVPHFK--FPGTKYIIDEPEYEDPR	619
Qy	592	AVREPAKETIDSCVKIDQVYAGEFGEVCSGHLKDPGKREIYVAKITLKSSTTEQORDP	651
Db	620	AVHOFKAKELDASCIRIERYVAGCFEFGVCSGRKLTKGRDVAVALTKLVGTGEKORDF	679
Qy	652	LSBASIMQGFHPHVHLEGVYTKSPVMIITEFEMGSLDSFLTRONDQOFVIOYGLM	711
Db	680	LCBASIMQGFHPHVHLEGVYTRGRVMIIVIEFMENGALDAFLRKHDOQFVIOYGLM	739
Qy	712	RGIAAGMKYILDNNYVHRDLAARNILVNSMLVCVSDFGLSRFLLEDYDSDPTYTSALGSK	771
Db	740	RGIAAGMKYILADMGVYHRDLAARNILVNSMLVCVSDFGLSRIEED-PEAYITTT-GGK	797
Qy	772	FPRIKRTAPEAIQYKRFYSASVWSYGYVMVEWMSYGBRPVMDTNDQVINAIEQDYRLP	831
Db	798	IPVPRTAPEALQYRKFPYSASVWSYGYVMVEWMSYGBRPVMDSNQVILKALIEGBRILPA	857
Qy	832	PMDCSALHQLMLCQOKDRNHRPKFGQIYVNTLDDKRI RNPSISLKAAPASLSGINPLDR	891
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RESULT 15  
jc5672  
receptor tyrosine kinase (EC 2.7.-.-) Etk precursor - mouse  
N:Alternate names: developmental kinase 1  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Nov-1997 #sequence\_revision 20-Nov-1997 #text\_change 18-Jun-1998  
C:Accession: J05672; I4611; S1740  
R:Talukder, A.H.; Muramatsu, T.; Kaneda, N.  
Cell Struct. Funct. 22, 477-485, 1997.

A:Title: A novel/truncated variant form of Etk/MDKI receptor tyrosine kinase is expressed  
A:Reference number: J05672; MUID:96035156  
A:Accession: J05672  
A:Molecule type: mRNA  
A:Residues: 1-998 <TAL>  
A:Experimental source: embryo  
R:Closssek, T.; Millauer, B.; Ullrich, A.  
Oncogene 9, 97-106, 1995  
A:Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel  
A:Reference number: 148611  
A:Accession: 148611  
A:Status: preliminary; translated from GR/EMBL/DBST  
A:Molecule type: mRNA  
A:Residues: 1-998 <RES>  
A:Cross-references: EMBL:X79082; NID:9607133; PIDN:CAA55687.1; PID:9607134  
C:Comment: This enzyme plays a role during development involving differentiation and pnc  
C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat  
C:Keywords: Aty; brain; phosphotransferase; transmembrane protein  
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F:441-534/Domain: fibronectin type III repeat <FN2>  
F:554-579/Domain: transmembrane #status predicted <TM>  
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F:639-647/Region: protein kinase ATP-binding motif  
F:920-986/Domain: SAM homology <SAM>

Query Match	58.7%	Score 3001;	DB 2;	Length 998;
Best Local Similarity	58.6%	Pred NO	3 08-124	

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OY 63 FIRRGAHRIRIHEKMSVRDCSSIPSVSGCKEFTFNLYEADDPDSAKTPEPMENWV 122
Db 89 WISGMNQRIVELKTLRDCNSLPGVLGTCKEFTFNLYETDWD---TGRNIRENLV 144
OY 123 KYDTIADDESQVLDLGRVWKINTEVRSFCPSVRSGFYLAFOBYGCMSLIARVEFYRK 182
Db 145 KIDTIADDESFQODLERKMKLNTVEIRIELPSLKGIFYLAFQDVGACIALVSVKYYKK 204
OY 183 CPRIIONGAIQEOELTSGESFSLVAAGSCILANA-EEDVYIKLYCNGDEGMLVPIGRCM 241
Db 205 CMTIYELNLAFPDVTIISERSLSLEVGTCCSSAAEEEAENSPRHCKSAEGEMLPIGKCI 264
OY 242 CKAGFEAVENGTVCRGCPSTGFKNQODEACTHCPINSRTSEGATNCVCNGEYRYADLD 301
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Db 323 PYYVACIRPSPAPONLFFNINOTTVSLEMSPPADNGGRNDVTYIILCKRCSEWGECVPC 382
OY 362 GDNVQVAPROGLTEPRITISDLIAHQYFEEIOAVNGSYDQSPFSQAFSANTITNOAA 421
Db 383 GSNIGWPMQOTGLEDNVYMDLIAHANTFEEVAVANGVSDLSORSRLFAAVSLITTOAA 442
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Db 443 PSQOVSGMKERVLQORSVQLSMOPEBHNQYITEEIEIKYKDKQREKRYTSLTKRSTASI 502
OY 480 TGLKAGIYVFOVARIVAGYGRYSGMFIQYMTA-----EYOTSIOEKLPITIGS-S 532
Db 503 NNKRGCTIVYEQIRAYTAAGYGNVSPRLDVAITLEBASGKMEFATAVSSSEONPVIIIAVVA 562
OY 533 AAGVELLIANVIAIYCNRR-GEFARDESYTDKLOHNTSGHITPMKMIYIDPTEYEDPNE 591
Db 563 VAGTILVENVFETIIGRRHRCIGSKADOEDDELYHFHFK---FPGTYIYIDPEYEDPNR 619

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Qy	592	AYREPKEDIDSCVILIEOYIANGEGEYECSHLIPGKREIIEVAIKTLKSGYTEKORDF	651
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Qy	652	LSEASIMGOFDHPNVIHLEGVYKTFPMITTERMENGSLDSEFLRONDGOFYIOLVGM	711
Db	680	LEASIMGOFDHPNVHLEGVYTKRKPMAIIEEMGALDAEFLRKIDGOFYIOLVGM	739
Qy	712	KRIIAAGMKYIADMNIVHRLAARNILVNSLNCVSDPFGLSRPLEDDTSPFTYSALGK	771
Db	740	RRIAGMRRLADMGVYHRDLAARNILVNSLNCVSDPFGLSRVIDE - PEAVYTTT - GSK	797
Qy	772	PIIRMTAPEALQYRKFTSASDVMSYGYIWMVMSYGERPYMDMTNODVINAIEDYRLRP	831
Db	798	IVRRMTAPEALQYRKFTSASDVMSYGYIWMVMSYGERPYMDMSNOBIVAIIEGYRLPA	857
Qy	832	PMDCCSAHLQIILDCWKOKDRHHRKFCQIYVTTLDKMLRNNSLX - - - - - AMAPLSSGIN	886
Db	858	PMDCPAGLHQIILDCWKOKDRAREKFKEQIYGLIDKMLRNNSLXKTPLGTCRPLS - - - - -	912
Qy	887	PLLDRTIDYSEMTVDEMLEAIKMGYKESFANAGFTSPDYVSOMMEDIILRVYTLG	946
Db	913	PLLDSTDFEAFCSVGEVMOQAIKMEYRKDNFTAAAGNSLESVARMHTIDVMSLTITLG	972
Qy	947	HOKTIMSIOTVRAOM	962
Db	973	HOKTIMSIOTVRAOM	988

Search completed: July 24, 2001, 16:29:36  
Job time: 227 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2001, 16:30:39 ; Search time 16.22 Seconds  
(without alignments)  
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Title: US-09-378-759-11

Sequence: 1 LLAVEETLMDSTTATAEIG.....ILNSIQVRAQMNQIQSV 970

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 193259 seqs, 20144635 residues

Word size : 0

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*
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- 4: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*
- 6: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	970	100.0	970	2	US-08-449-645A-11
2	970	100.0	970	2	US-08-702-367A-11
3	970	100.0	970	5	PCT-US95-04681-11
4	322	33.2	994	4	US-08-542-635-2
5	103	10.6	995	1	US-08-162-809-18
6	103	10.6	995	2	US-08-673-789-5
7	103	10.6	1011	1	US-08-162-809-12
8	40	4.1	998	2	US-08-449-645A-17
9	40	4.1	998	2	US-08-702-367A-17
10	40	4.1	998	5	PCT-US95-04681-17
11	40	4.1	998	5	PCT-US96-00419-2
12	39	4.0	59	1	US-08-222-616-25
13	39	4.0	59	2	PCT-US95-04228-25
14	37	3.8	57	2	US-08-456-647B-10
15	37	3.8	57	2	US-08-237-789-11
16	36	3.7	612	2	US-08-673-789-11
17	36	3.7	973	1	US-08-162-809-8
18	35	3.6	970	2	US-08-673-789-7
19	35	3.6	973	1	US-08-162-809-10
20	35	3.6	988	1	US-08-162-809-14
21	35	3.6	993	1	US-08-348-143-1
22	35	3.6	993	1	US-08-571-785-1
23	35	3.6	998	2	US-08-449-645A-20
24	35	3.6	998	2	US-08-702-367A-20
25	35	3.6	998	5	PCT-US95-04681-20
26	32	3.3	951	1	US-08-162-809-2
27	31	3.2	687	2	US-08-449-645A-29

28	31	3.2	687	2	US-08-702-367A-29	Sequence 29, Appl
29	31	3.2	849	1	US-08-162-809-6	Sequence 10, Appl
30	31	3.2	849	2	US-08-673-789-10	Sequence 6, Appl
31	31	3.2	984	3	US-08-673-789-6	Sequence 3, Appl
32	31	3.2	986	2	US-08-673-789-3	Sequence 15, Appl
33	31	3.2	986	2	US-08-449-645A-15	Sequence 15, Appl
34	31	3.2	986	2	US-08-702-367A-15	Sequence 15, Appl
35	31	3.2	986	5	PCT-US95-04681-15	Sequence 15, Appl
36	31	3.2	987	1	US-08-436-044-6	Sequence 6, Appl
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38	31	3.2	987	5	PCT-US95-08812-36	Sequence 6, Appl
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41	31	3.2	1276	1	US-08-222-616-24	Sequence 24, Appl
42	31	3.2	1276	5	PCT-US95-04228-24	Sequence 24, Appl
43	30	3.1	976	2	US-08-449-645A-18	Sequence 18, Appl
44	30	3.1	976	2	US-08-702-367A-18	Sequence 18, Appl
45	30	3.1	976	5	PCT-US95-04681-18	Sequence 18, Appl

# ALIGNMENTS

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RESULT 1
US-08-449-645A-11
; Sequence 11, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645A-11

Query Match 100.0%; Score 970; DB 2; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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181 RRCPRRIIONGALFQETLSGAESTSLVAANGSCIANAEVDVPIKLYCNGDGEVLVPIGR 240
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RESULT 2
US-08-702-367A-11
; Sequence 11, Application us/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBM
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks

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STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702.367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-11

Query Match      100.0%; Score 970; DB 2; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 DPLDMCCTTIPSAPOAVISSVNETSLMLEMTPPRDSGREDLVYNTICKSCSGRGACTR 360
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361 CGDNVOYAPROGLTEPRRIYISDLAHTQYTEIQAANGVTDDSPSPQFASVNTTNOA 420
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421 APSAASIMHOVSTVDSITLSMSQDPQNGVILIDYELQYERKELSEYNATAIKSPNTYT 480
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481 GLKAGAIYFQVARTVAGYGRYSGKMFOTMTEAEYQTSIOEKLPLIGSSAAGLVFLI 540
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Db 721 LADMNVYHDLAARNILVNSNLCKVSDGLSRFLEDDPSDPTYSALGCKRPPIRTAPE 780
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Db 781 AIQYRKFTSASDVWSYGIYMWEMVSYGERPYDMTNQDVINAIEDDYRLPPMDCPSALH 840
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## RESULT 3

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PCT-US95-04681-11
Sequence 11, Application PC/TUS9504681
GENERAL INFORMATION:

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APPLICANT: Fox, Gary M.
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESS: Amgen Patent Operations/NBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SRO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-11

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Query Match 100.0%; Score 970; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLAAVEETLNDSTATATFELGMVYHPPSGMEVSGYDENMNTITTYOVCNFFESSQNNMLR 60
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Db 121 WVKVDITIADESFQVDLGRVAKINTEVRSFGVSRSGFYLAFOYGGCMLIAVREY 180
QY 181 RCPRIIONGAIIEQETLSGAEASTSLVAAAGSCIANAEVDPIKLYCNGDGEWLPIGRC 240
Db 181 RCPRIIONGAIIEQETLSGAEASTSLVAAAGSCIANAEVDPIKLYCNGDGEWLPIGRC 240
QY 241 MCKAGFEAVENGIVCRKCPGSGTFKANOGEACHTCPINSRTSGATNCVCRCNGYRADL 300
Db 241 MCKAGFEAVENGIVCRKCPGSGTFKANOGEACHTCPINSRTSGATNCVCRCNGYRADL 300
QY 301 DPLMPCCTTIPSAPOAVISSVNETSLMLEWTPPHDSGREDLYNINICKSCGSGRACR 360
Db 301 DPLMPCCTTIPSAPOAVISSVNETSLMLEWTPPHDSGREDLYNINICKSCGSGRACR 360
QY 361 CGDNVOYAPRQGLGTEBRITISDLAHTQYTFEIOAVNGVTIDSPSPQFASVNIITNQA 420
Db 361 CGDNVOYAPRQGLGTEBRITISDLAHTQYTFEIOAVNGVTIDSPSPQFASVNIITNQA 420
QY 421 APSAVSIMHOVSRTVDSITLSMSQPDOPNGVILDYELQYIEKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHOVSRTVDSITLSMSQPDOPNGVILDYELQYIEKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYFQVARRIVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIGSSAAGLVFLI 540
Db 481 GLKAGAIYFQVARRIVAGYGRYSGKMYFQMTAEAYQTSIQEKLPLIGSSAAGLVFLI 540
QY 541 AVVYIAIVCNRRGERADSEYTDKLOHTYSGHTTPGKTIYIDPFTTEDNEAREPAKET 600
Db 541 AVVYIAIVCNRRGERADSEYTDKLOHTYSGHTTPGKTIYIDPFTTEDNEAREPAKET 600
QY 601 DISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORPDFSEASIMGO 660
Db 601 DISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORPDFSEASIMGO 660
QY 661 FDHPNVIHLEGVYTKSTPWIIITEFMENGLSDSFLRQNDGQFTVIQVGMRLGIAAGMKY 720
Db 661 FDHPNVIHLEGVYTKSTPWIIITEFMENGLSDSFLRQNDGQFTVIQVGMRLGIAAGMKY 720
QY 721 LADMNVYHDLAARNILVNSNLCKVSDGLSRFLEDDPSDPTYSALGCKRPPIRTAPE 780
Db 721 LADMNVYHDLAARNILVNSNLCKVSDGLSRFLEDDPSDPTYSALGCKRPPIRTAPE 780
QY 781 AIQYRKFTSASDVWSYGIYMWEMVSYGERPYDMTNQDVINAIEDDYRLPPMDCPSALH 840
Db 781 AIQYRKFTSASDVWSYGIYMWEMVSYGERPYDMTNQDVINAIEDDYRLPPMDCPSALH 840
QY 841 QLMDCWOKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSGILNPLDRTIPDYTSFN 900
Db 841 QLMDCWOKDRNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSGILNPLDRTIPDYTSFN 900
QY 901 TYDENVLEAIKMGQYKESFANAGFTSFDVYSQMMEDILRVGVTLAGHOKKILNSIQVWRA 960
Db 901 TYDENVLEAIKMGQYKESFANAGFTSFDVYSQMMEDILRVGVTLAGHOKKILNSIQVWRA 960
QY 961 QMNOIOSVEY 970
Db 961 QMNOIOSVEY 970

```

## RESULT 4

```

US-08-542-635-2
Sequence 2, Application US/08542635
Patent No. 6218356
GENERAL INFORMATION:

```

```

APPLICANT: Pawson, Anthony
APPLICANT: Henkemeyer, Mark
APPLICANT: Letwin, Kenneth
TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESS: Bereskin & Parr

```

STREET: 40 King Street West, Box 401  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/542,635  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McDiarmid, Shona S.  
REGISTRATION NUMBER: 38,798  
REFERENCE/DOCKET NUMBER: 3153-162  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 364-7311  
TELEFAX: (416) 361-1398  
TELEX: 06-23115  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
DEVELOPMENTAL STAGE: Embryo  
IMMEDIATE SOURCE:  
LIBRARY: lambda gt10 cDNA library  
CLONE: Combined pNukRae A2 and K2 and cDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Distal end of chromosome 4  
MAP POSITION: near the and-1 mutation  
US-08-542-635-2

Query Match 33.2%; Score 322; DB 4; Length 994;  
Best Local Similarity 100.0%; Pred. No. 1.8e-286;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 159 GFYIAFDYGGCMLIAVRVYRRCPRITQNGAIFQETLSAESTSVYARGSCINAAEE 218  
DB 181 GFYIAFDYGGCMLIAVRVYRRCPRITQNGAIFQETLSAESTSVYARGSCINAAEE 240  
QY 219 VDVPIKLYCNGDGMVLPDGRGCMKAGFEAVENGTVRCGSPGTFKANOGEACTHCPIN 278  
DB 241 VDVPIKLYCNGDGMVLPDGRGCMKAGFEAVENGTVRCGSPGTFKANOGEACTHCPIN 300  
QY 279 SRTTSEGATNCVCRNGYRRADLDLDMPCCTTIPSAPOAVISVNETSLMLFWTPRRSGG 338  
DB 301 SRTTSEGATNCVCRNGYRRADLDLDMPCCTTIPSAPOAVISVNETSLMLFWTPRRSGG 360  
QY 339 REDLYNITICSCGSGRACRRCNDNOYARROIGTEPRITVSDLAHTQYTEIQAVN 398  
DB 361 REDLYNITICSCGSGRACRRCNDNOYARROIGTEPRITVSDLAHTQYTEIQAVN 420  
QY 399 GVTDOSPSPQFASVNTITNOAASAVSIMHOVSRVDSITLMSOPDQNGVILDYELQ 458  
DB 421 GVTDOSPSPQFASVNTITNOAASAVSIMHOVSRVDSITLMSOPDQNGVILDYELQ 480  
QY 459 YYEKELSEYNATAIKSPNTVT 480  
DB 481 YYEKELSEYNATAIKSPNTVT 502

RESULT 5  
US-08-162-809-18  
Sequence 18, Application US/08162809

Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Sajjadi, Pereydon G.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 995 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-809-18

Query Match 10.6%; Score 103; DB 1; Length 995;  
Best Local Similarity 100.0%; Pred. No. 6.5e-86;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 574 TPGMKIYIDPFTYEDPNEAVREFAKETIDISCVKIEQVITAGERGEVCSGHLTPKREIF 633  
DB 599 TPGMKIYIDPFTYEDPNEAVREFAKETIDISCVKIEQVITAGERGEVCSGHLTPKREIF 658  
QY 634 VAIKTKSGYTEKORDPLSEASIMGOFDPNVIHLEGVTKS 676  
DB 659 VAIKTKSGYTEKORDPLSEASIMGOFDPNVIHLEGVTKS 701

RESULT 6  
US-08-673-789-5  
Sequence 5, Application US/08673789  
Patent No. 5814479  
GENERAL INFORMATION:  
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,  
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,  
APPLICANT: GEORGE, F.  
TITLE OF INVENTION: BSK RECEPTOR LIKE  
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR  
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/673,789  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/177,812  
FILING DATE: 04-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 995  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
US-08-673-789-5

Query Match 10.6%; Score 103; DB 2; Length 995;  
Best Local Similarity 100.0%; Pred. No. 6,5e-86;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIF 633  
DB 599 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIF 658  
QY 634 VAIKTLKSGYTEKORRDLSEASIMGQFDHPNVIHLEGVYTKS 676  
DB 659 VAIKTLKSGYTEKORRDLSEASIMGQFDHPNVIHLEGVYTKS 701

## RESULT 7

US-08-162-809-12  
Sequence 12, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1011 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-809-12

Query Match 10.6%; Score 103; DB 1; Length 1011;  
Best Local Similarity 100.0%; Pred. No. 6,6e-86;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIF 633  
DB 615 TPGMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRKEIF 674  
QY 634 VAIKTLKSGYTEKORRDLSEASIMGQFDHPNVIHLEGVYTKS 676  
DB 675 VAIKTLKSGYTEKORRDLSEASIMGQFDHPNVIHLEGVYTKS 717

## RESULT 8

US-08-449-645A-17  
Sequence 17, Application US/08449645A  
Patent No. 5981245  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,645A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-449-645A-17

Query Match 4.1%; Score 40; DB 2; Length 998;  
Best Local Similarity 100.0%; Pred. No. 3,2e-28;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RMTAPEAIQYRKFTSASDVSYGIVMEVNSYGERPYMD 814  
DB 801 RMTAPEAIQYRKFTSASDVSYGIVMEVNSYGERPYMD 840

## RESULT 9

US-08-702-367A-17  
Sequence 17, Application US/08702367A  
Patent No. 5981246

GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehaven Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-367A-17

Query Match 4.1%; Score 40; DB 2; Length 998;  
Best Local Similarity 100.0%; Pred. No. 3.2e-28;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 814  
|||||  
DB 801 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 840

RESULT 10  
PCT-US95-04681-17  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehaven Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04681  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-04681-17

Query Match 4.1%; Score 40; DB 5; Length 998;  
Best Local Similarity 100.0%; Pred. No. 3.2e-28;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 814  
|||||  
DB 801 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 840

RESULT 11  
PCT-US96-00419-2  
GENERAL INFORMATION:  
APPLICANT: Thomas Closssek, Axel Ullrich, Birgit  
ATTORNEY/AGENT INFORMATION:  
NAME: Millaue  
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/00419  
FILING DATE: January 3, 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US96-00419-2

Query Match 4.1%; Score 40; DB 5; Length 998;  
Best Local Similarity 100.0%; Pred. No. 3.2e-28;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 814  
|||||  
DB 801 RWTAPPAIOYRKFTSASDVWSYGIWMEVWSYGERPYWDM 840

RESULT 12  
US-08-222-616-25



ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: 07251/007002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 57 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-456-647B-10

Query Match 3.8%; Score 37; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.5e-26;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 NILVNSNLVCKVSDRGLSRFLDDTSDPTYSALGSK 771  
Db 1 NILVNSNLVCKVSDRGLSRFLDDTSDPTYSALGSK 37

RESULT 15  
US-08-237-401A-10  
Sequence 10, Application US/08237401A  
Patent No. 5637448  
GENERAL INFORMATION:  
APPLICANT: Lemke Ph.D. et al., Greg E.  
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/237,401A  
FILING DATE: 02-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/884,486  
FILING DATE: 15-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07251/007001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 57 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-237-401A-10

Query Match 3.8%; Score 37; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.5e-26;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 NILVNSNLVCKVSDRGLSRFLDDTSDPTYSALGSK 771

Db 1 NILVNSNLVCKVSDRGLSRFLDDTSDPTYSALGSK 37

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Wed Jul 25 13:03:50 2001

us-09-378-759-11.oli.ra1

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:32:19 ; Search time 53.59 Seconds

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Title: US-09-378-759-11

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Gapop 60.0 , Gapext 60.0

Searched: 1316263 seqs, 17692484 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1316263

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*  
22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	970	100.0	970	8 US-08-449-645-11	Sequence 11, Appl
2	970	100.0	970	11 US-08-702-367-11	Sequence 11, Appl
3	970	100.0	970	17 US-09-378-759-11	Sequence 11, Appl
4	490	50.5	524	11 US-08-730-700A-7	Sequence 7, Appl
5	322	33.2	984	6 US-08-235-407-2	Sequence 2, Appl
6	322	33.2	984	11 US-08-727-463-2	Sequence 2, Appl
7	322	33.2	984	11 US-08-727-463-2	Sequence 2, Appl
8	322	33.2	994	11 US-08-730-700A-2	Sequence 2, Appl
9	322	33.2	994	11 US-08-730-700A-2	Sequence 2, Appl
10	198	20.4	551	23 US-60-206-600-138	Sequence 138, App

11	198	20.4	551	23	US-60-208-965-196	Sequence 196, App
12	111	11.4	191	23 <td>US-60-233-606-78</td> <td>Sequence 78, Appl</td>	US-60-233-606-78	Sequence 78, Appl
13	98	10.1	162	23 <td>US-60-248-798-295</td> <td>Sequence 295, Appl</td>	US-60-248-798-295	Sequence 295, Appl
14	83	8.6	84	23 <td>US-60-160-202-4014</td> <td>Sequence 4014, Ap</td>	US-60-160-202-4014	Sequence 4014, Ap
15	83	8.6	94	23 <td>US-60-160-209-3395</td> <td>Sequence 3395, Ap</td>	US-60-160-209-3395	Sequence 3395, Ap
16	83	8.6	149	23 <td>US-60-169-868-4968</td> <td>Sequence 4968, Ap</td>	US-60-169-868-4968	Sequence 4968, Ap
17	83	8.6	173	23 <td>US-60-196-713-3263</td> <td>Sequence 3263, Ap</td>	US-60-196-713-3263	Sequence 3263, Ap
18	83	8.6	179	23 <td>US-60-187-380-108</td> <td>Sequence 108, App</td>	US-60-187-380-108	Sequence 108, App
19	83	8.6	179	23 <td>US-60-187-412-391</td> <td>Sequence 391, App</td>	US-60-187-412-391	Sequence 391, App
20	82	8.5	83	23 <td>US-60-160-202-4070</td> <td>Sequence 4070, Ap</td>	US-60-160-202-4070	Sequence 4070, Ap
21	82	8.5	83	23 <td>US-60-160-209-4085</td> <td>Sequence 4085, Ap</td>	US-60-160-209-4085	Sequence 4085, Ap
22	65	6.7	84	23 <td>US-60-202-183-289</td> <td>Sequence 289, App</td>	US-60-202-183-289	Sequence 289, App
23	51	5.3	69	23 <td>US-60-192-733-3058</td> <td>Sequence 3058, Ap</td>	US-60-192-733-3058	Sequence 3058, Ap
24	51	5.3	69	23 <td>US-60-194-091-1122</td> <td>Sequence 1122, Ap</td>	US-60-194-091-1122	Sequence 1122, Ap
25	51	5.3	69	23 <td>US-60-194-091-1122</td> <td>Sequence 1122, Ap</td>	US-60-194-091-1122	Sequence 1122, Ap
26	42	4.3	48	23 <td>US-60-163-232-1903</td> <td>Sequence 1903, Ap</td>	US-60-163-232-1903	Sequence 1903, Ap
27	42	4.3	48	23 <td>US-60-163-232-1903</td> <td>Sequence 1903, Ap</td>	US-60-163-232-1903	Sequence 1903, Ap
28	41	4.2	41	23 <td>US-60-162-245-2293</td> <td>Sequence 2293, Ap</td>	US-60-162-245-2293	Sequence 2293, Ap
29	41	4.2	41	23 <td>US-60-163-233-3570</td> <td>Sequence 3570, Ap</td>	US-60-163-233-3570	Sequence 3570, Ap
30	40	4.1	44	23 <td>US-60-205-167-143</td> <td>Sequence 143, App</td>	US-60-205-167-143	Sequence 143, App
31	40	4.1	47	23 <td>US-60-198-828-574</td> <td>Sequence 574, App</td>	US-60-198-828-574	Sequence 574, App
32	40	4.1	56	23 <td>US-60-170-373-2238</td> <td>Sequence 2238, Ap</td>	US-60-170-373-2238	Sequence 2238, Ap
33	40	4.1	56	23 <td>US-60-170-374-1936</td> <td>Sequence 1936, Ap</td>	US-60-170-374-1936	Sequence 1936, Ap
34	40	4.1	529	11 <td>US-08-730-700A-11</td> <td>Sequence 11, Appl</td>	US-08-730-700A-11	Sequence 11, Appl
35	40	4.1	933	7 <td>US-08-368-776A-11</td> <td>Sequence 11, Appl</td>	US-08-368-776A-11	Sequence 11, Appl
36	40	4.1	934	7 <td>US-08-368-776A-12</td> <td>Sequence 12, Appl</td>	US-08-368-776A-12	Sequence 12, Appl
37	40	4.1	998	7 <td>US-08-368-776-2</td> <td>Sequence 2, Appl</td>	US-08-368-776-2	Sequence 2, Appl
38	40	4.1	998	8 <td>US-08-449-645-17</td> <td>Sequence 17, Appl</td>	US-08-449-645-17	Sequence 17, Appl
39	40	4.1	998	11 <td>US-08-702-367-17</td> <td>Sequence 17, Appl</td>	US-08-702-367-17	Sequence 17, Appl
40	40	4.1	988	17 <td>US-09-378-759-17</td> <td>Sequence 17, Appl</td>	US-09-378-759-17	Sequence 17, Appl
41	39	4.0	59	6 <td>US-08-256-769B-36</td> <td>Sequence 36, Appl</td>	US-08-256-769B-36	Sequence 36, Appl
42	39	4.0	59	8 <td>US-08-446-648-25</td> <td>Sequence 25, Appl</td>	US-08-446-648-25	Sequence 25, Appl
43	39	4.0	59	11 <td>US-08-770-449-25</td> <td>Sequence 25, Appl</td>	US-08-770-449-25	Sequence 25, Appl
44	38	3.9	60	23 <td>US-60-187-412-271</td> <td>Sequence 271, App</td>	US-60-187-412-271	Sequence 271, App
45	38	3.9	63	23 <td>US-60-186-661-285</td> <td>Sequence 285, App</td>	US-60-186-661-285	Sequence 285, App

#### ALIGNMENTS

RESULT 1  
US-08-449-645-11  
Sequence 11, Application US/08449645  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
APPLICANT: Welch, Andrew A.  
APPLICANT: Jing, Shuguan  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,645  
FILING DATE: May 24, 1995  
CLASSIFICATION: A35  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287-A  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
us-08-449-645-11

Query Match 100.0%; Score 970; DB 8; Length 970;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TKIRRGGAHRIHVEKFSVRDCCSIPSPGSKETFNLYYEADDSATKTFPMNMENP 120
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DB 241 MCKAGEEAVENGIVCGCGSPGTFKANOGDEACTHCPINSRTTSEGAFTNCVCRNGYRADL 300
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DB 301 DPLDMCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNTICKSCSGRGACTR 360
QY 361 CGGNVOYAPRQLGLTEPRITISDLAHTQYTFEIOAVNGVTDDSPSPQASVNTITNQA 420
DB 361 CGGNVOYAPRQLGLTEPRITISDLAHTQYTFEIOAVNGVTDDSPSPQASVNTITNQA 420
QY 421 APSAVSITMHOVSRTVDSITLSMSGPOPOPNGLIDYELQYKEKLESEYNATAIKSPNTVA 480
DB 421 APSAVSITMHOVSRTVDSITLSMSGPOPOPNGLIDYELQYKEKLESEYNATAIKSPNTVA 480
QY 481 GLKAGALYVEQVBARFVAGYGRYSGKMYFQTMTEAEYQTSIOEKRLPLITGSSAAGLVFLI 540
DB 481 GLKAGALYVEQVBARFVAGYGRYSGKMYFQTMTEAEYQTSIOEKRLPLITGSSAAGLVFLI 540
QY 541 AVVYVIAVCCRGRPERADSEYTKLOHYTSGHTTPGKTIYIDPEYEDPNEAVERFAKEI 600
DB 541 AVVYVIAVCCRGRPERADSEYTKLOHYTSGHTTPGKTIYIDPEYEDPNEAVERFAKEI 600
QY 601 DISCVKIEQYIGAGEFEGEYVSGHKLPGKREIFAIAKTLKSGYTEKORDFLSEASIMGO 660
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DB 721 LADNNVYHRDLAARNILVNSNLVKVSDPGLSRFLLEDYDIPYTSALGKFKPLRMTAPE 780
QY 781 AIQYRKFTSASDVMSYGIIVMEVMSYGERPYWMTNDVINAIEQDVRLLPMDPCSAHL 840
DB 781 AIQYRKFTSASDVMSYGIIVMEVMSYGERPYWMTNDVINAIEQDVRLLPMDPCSAHL 840
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DB 841 QLMALDCQKORNRHPRKFGQIVNTLDKMTIRNPNSIKAMAPLSSGGINLPDLDRITPDYTSFN 900
QY 901 TVDEMLEAIMGQYKESFANAAGTFSPDVVSOMMEDILRQVNTLAGQKKILNSIOVMA 960
DB 901 TVDEMLEAIMGQYKESFANAAGTFSPDVVSOMMEDILRQVNTLAGQKKILNSIOVMA 960

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QY 961 QMNOIOSVEV 970  
DB 961 QMNOIOSVEV 970

## RESULT 2

us-08-702-367-11  
Sequence 11, Application US/08702367

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/229, 509

FILING DATE: 15-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

us-08-702-367-11

Query Match 100.0%; Score 970; DB 11; Length 970;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TKIRRGGAHRIHVEKFSVRDCCSIPSPGSKETFNLYYEADDSATKTFPMNMENP 120
QY 121 WVKVDITIADESFQYDLGGRVVKINTEVRSFGPVSRSGFYLAFODYGCMSLIAVRVY 180
DB 121 WVKVDITIADESFQYDLGGRVVKINTEVRSFGPVSRSGFYLAFODYGCMSLIAVRVY 180
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DB 181 RKCPRITLQNGATFOETLSGAESTSLVAANGSCIANAEVDVPKILYCNDDGEMLVPIGR 240
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DB 241 MCKAGEEAVENGIVCGCGSPGTFKANOGDEACTHCPINSRTTSEGAFTNCVCRNGYRADL 300
QY 301 DPLDMCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNTICKSCSGRGACTR 360
DB 301 DPLDMCCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNTICKSCSGRGACTR 360
QY 361 CGGNVOYAPRQLGLTEPRITISDLAHTQYTFEIOAVNGVTDDSPSPQASVNTITNQA 420

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Db 361 CGDNVOYARQLGTEPRRIYISDLAHTQYTEIQAAMKVTOQSPSPQFASVNTTNOA 420
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Db 421 APSAVSIMHOVSRTVDSITLSMSQDPQNGVILIDYELQYKEKELSEYNATAKSPNTVT 480
Qy 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQJMTAEAYOTSIOEKPLIIGSSAAGLVFLI 540
Db 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQJMTAEAYOTSIOEKPLIIGSSAAGLVFLI 540
Qy 541 AVVVAIAYCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDPNEAVREFAKEI 600
Db 541 AVVVAIAYCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDPNEAVREFAKEI 600
Qy 601 DISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDPFLSEASIMQO 660
Db 601 DISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDPFLSEASIMQO 660
Qy 661 FDHPNVIHLEGVYTKSTPMIITEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
Db 661 FDHPNVIHLEGVYTKSTPMIITEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
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Db 721 LADMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDTPSPITYSALGKFPRIKTAPE 780
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Db 781 AIQYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLPRPMDCPSALH 840
Qy 841 QLMDCQKDRNHRPKFGQIYVNTLDKMIIRNPNSLKAMAPLSSGINPLDRTIDYTSFN 900
Db 841 QLMDCQKDRNHRPKFGQIYVNTLDKMIIRNPNSLKAMAPLSSGINPLDRTIDYTSFN 900
Qy 901 TVDEWLEAIKMGQYKESFANAGFTSFVDVVSQMMEDILRVGVTLAGHOKKLINSIQWRA 960
Db 901 TVDEWLEAIKMGQYKESFANAGFTSFVDVVSQMMEDILRVGVTLAGHOKKLINSIQWRA 960
Qy 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

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; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; us-09-378-759-11

Query Match      100.0%; Score 970; DB 17; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LLAVEETLMDSTATATLELGMVHPSPGMEVSVSDYDNMNTIRIYQVCNPFESSONMLR 60
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Db 61 TKFIRRGARHRIHEMKEFSVRDCSSIPSPGCKETFNLYYEADFDSATKTPNNMNEP 120
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Db 361 CGDNVOYARQLGTEPRRIYISDLAHTQYTEIQAAMKVTOQSPSPQFASVNTTNOA 420
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Db 421 APSAVSIMHOVSRTVDSITLSMSQDPQNGVILIDYELQYKEKELSEYNATAKSPNTVT 480
Qy 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQJMTAEAYOTSIOEKPLIIGSSAAGLVFLI 540
Db 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQJMTAEAYOTSIOEKPLIIGSSAAGLVFLI 540
Qy 541 AVVVAIAYCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDPNEAVREFAKEI 600
Db 541 AVVVAIAYCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFYEDPNEAVREFAKEI 600
Qy 601 DISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDPFLSEASIMQO 660
Db 601 DISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKQRDPFLSEASIMQO 660
Qy 661 FDHPNVIHLEGVYTKSTPMIITEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
Db 661 FDHPNVIHLEGVYTKSTPMIITEFMENGSLDSFLRQNDGQFTYVQLVGMRLGIAAGKY 720
Qy 721 LADMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDTPSPITYSALGKFPRIKTAPE 780
Db 721 LADMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDTPSPITYSALGKFPRIKTAPE 780
Qy 781 AIQYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLPRPMDCPSALH 840
Db 781 AIQYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNDQVINAIEDYRLPRPMDCPSALH 840
Qy 841 QLMDCQKDRNHRPKFGQIYVNTLDKMIIRNPNSLKAMAPLSSGINPLDRTIDYTSFN 900
Db 841 QLMDCQKDRNHRPKFGQIYVNTLDKMIIRNPNSLKAMAPLSSGINPLDRTIDYTSFN 900

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QY 901 TVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRVGTLAGHOKKILNSIOVMRA 960  
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| | | | |  
QY 961 OMNOIOSVEV 970  
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DB 961 OMNOIOSVEV 970  
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RESULT 4  
US-08-730-700A-7  
; Sequence 7, Application US/08730700A  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeyer, Mark  
; TITLE OF INVENTION: Method of Activating a Novel Ligand  
; TITLE OF INVENTION: Regulatory Pathway  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Room 970  
; STREET: 600 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1X5  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/730,700A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,518  
; FILING DATE: 13-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurdzyk, Linda M.  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-196  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 416-586-3235  
; TELEFAX: 416-586-3110  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 524 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-730-700A-7  
Query Match 50.5%; Score 490; DB 11; Length 524;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | |  
QY 541 AVVYIAIVCNRRGFERADSETYDKLQHTSGHTPGMKIYIDPTYDDPNVAVEFAKEI 600  
| | | | |  
DB 95 AVVYIAIVCNRRGFERADSETYDKLQHTSGHTPGMKIYIDPTYDDPNVAVEFAKEI 154  
| | | | |  
QY 601 DISCVKIEOVYAGGEPFGVSGHKLPGKRIFAATIKLSGYEKORPDLSEASIMQ 660  
| | | | |  
DB 155 DISCVKIEOVYAGGEPFGVSGHKLPGKRIFAATIKLSGYEKORPDLSEASIMQ 214  
| | | | |  
QY 661 FDHBNVTHLEGVYTKSTPVMTTEFMENGSLDSFLRNDGQFTVIQVGLMGLGIAAGMKY 720  
| | | | |

DB 215 FDHBNVTHLEGVYTKSTPVMTTEFMENGSLDSFLRNDGQFTVIQVGLMGLGIAAGMKY 274  
| | | | |  
QY 721 LADNMYVHRLDAARNILVNSNLVCKVSDGLSRFLEDDTSPTYSALGKFPTRMAPE 780  
| | | | |  
DB 275 LADNMYVHRLDAARNILVNSNLVCKVSDGLSRFLEDDTSPTYSALGKFPTRMAPE 334  
| | | | |  
QY 781 AIOYKFTSASDVMSYGIYMEVMSYGERPYWDMTNDQVINAIDODRILPPMPCPSALH 840  
| | | | |  
DB 335 AIOYKFTSASDVMSYGIYMEVMSYGERPYWDMTNDQVINAIDODRILPPMPCPSALH 394  
| | | | |  
QY 841 QLMDCMOKDRNHRPFQGIYVNTDKMIRNPNLSKAMAPLSSGINLPILDRTPDYTSFN 900  
| | | | |  
DB 395 QLMDCMOKDRNHRPFQGIYVNTDKMIRNPNLSKAMAPLSSGINLPILDRTPDYTSFN 454  
| | | | |  
QY 901 TVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRVGTLAGHOKKILNSIOVMRA 960  
| | | | |  
DB 455 TVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRVGTLAGHOKKILNSIOVMRA 514  
| | | | |  
QY 961 OMNOIOSVEV 970  
| | | | |  
DB 515 OMNOIOSVEV 524  
| | | | |

RESULT 5  
US-08-235-407-2  
; Sequence 2, Application US/08235407  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeyer, Mark  
; APPLICANT: Letwin, Kenneth  
; TITLE OF INVENTION: NOVEL NEURAL KINASE AND RECEPTOR  
; TITLE OF INVENTION: TYROSINE KINASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bereskin & Part  
; STREET: 40 King Street West, Box 401  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,407  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurdzyk, Linda M.  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-82  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 364-1398  
; TELEX: 06-23115  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 994 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
; DEVELOPMENTAL STAGE: Embryo  
; IMMEDIATE SOURCE:  
; LIBRARY: lambda gt10 cDNA library  
; CLONE: Combined pNURACE A2 and K2 and cDNA clones  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: Distal end of chromosome 4  
; MAP POSITION: near the and-1 mutation

US-08-235-407-2

```
Query Match      33.2%; Score 322; DB 6; Length 994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 0; Indels
```

Qy	159	GFYLAFODYGGCMLINAVREYRRCPRIOGALFQETLSGAESTSLVAARGSCIAAAE	218
Db	181	GFYLAFODYGGCMLINAVREYRRCPRIOGALFQETLSGAESTSLVAARGSCIAAAE	240
Qy	219	VDVPRKLYCNDGEMLPIPIGCMCKAGFEAVENCTVCRCPSGTFKXNCGDEACTHCPIN	278
Db	241	VDVPRKLYCNDGEMLPIPIGCMCKAGFEAVENCTVCRCPSGTFKXNCGDEACTHCPIN	300
Qy	279	SRTSSEGCATNCVCRNGYVRALDLDLDMPCTTIPSPAQAVISSVNETSLMLEWTPPRDSCG	338
Db	301	SRTSSEGCATNCVCRNGYVRALDLDLDMPCTTIPSPAQAVISSVNETSLMLEWTPPRDSCG	360
Qy	339	REDLYVNIITICKSCSGGRACRTRCGDNDQVYAROLGTEPRITYSDDLAAHYFTEIDAVN	398
Db	361	REDLYVNIITICKSCSGGRACRTRCGDNDQVYAROLGTEPRITYSDDLAAHYFTEIDAVN	420
Qy	399	GVTDDSPSPSPASVNIITNNOAASAVSIMHQSRTVDSITLSMSQDPDQNGVILDELO	458
Db	421	GVTDDSPSPSPASVNIITNNOAASAVSIMHQSRTVDSITLSMSQDPDQNGVILDELO	480
Qy	459	YXEKLSYNNATATKSPNTVT 480	
Db	481	YXEKLSYNNATATKSPNTVT 502	

RESULT 6  
US-08-727-463-2

; Sequence 2, Application US/08727463  
; GENERAL INFORMATION:

:  
:  
: APPLICANT: Pawson, Anthony  
:  
: APPLICANT: Henkemeyer, Mark  
:  
: APPLICANT: Letwin, Kenneth  
:  
: TITLE OF INVENTION: NEURAL RECEPTOR TYROSINE KINASES  
:  
: NUMBER OF SEQUENCES: 2  
:  
: CORRESPONDENCE ADDRESS:

1 ADDRESS: MERCHANT & GOULD  
2 STREET: 3100 Northwest Center, 90 South Seventh Street  
3 CITY: Minneapolis  
4 STATE: Minnesota  
5 COUNTRY: U.S.A.  
6 ZIP: 55403-4131  
7  
8 COMPUTER READABLE FORM:  
9 MEDIUM TYPE: Floppy disk  
10 COMPUTER: IBM PC compatible  
11 OPERATING SYSTEM: PC-DOS/MS-DOS  
12 SOFTWARE: PatentIn Release #1.0, Version #1.25  
13 CURRENT APPLICATION DATA:  
14 APPLICATION NUMBER: US/08/727,463  
15 FILING DATE: 18-OCT-1996

```

?
? DEVELOPMENTAL STAGE: Embryo
? IMMEDIATE SOURCE:
?
? LIBRARY: lambda gt10 cDNA library
?
? CLONE: Combined pINKRACE A2 and K2 and cDNA clones
?
? POSITION IN GENOME:
?
? CHROMOSOME/SEGMENT: Distal end of chromosome 4
?
? MAP POSITION: near the abd-1 mutation
?
US-08-727-463-2

```

Query Match	33.2%	Score 322:	DB 11;	length 994;
Best Local Similarity	100.0%	Pred. No.	0;	
Matches 322;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

QY	159	GFYLAFQDYGSCMSLIARVRYRRCPRIOGALFQETLSGAEBSSTLVAARGSCIANAE	218
Db	181	GFYLAFQDYGSCMSLIARVRYRRCPRIOGALFQETLSGAEBSSTLVAARGSCIANAE	240
QY	219	VDVPIKLYCNGDEMLVPIGCMCKKAGFEAVENSTVCRCGSPGFRKNOGDEACTHCIPIN	278
Db	241	VDVPIKLYCNGDEMLVPIGCMCKKAGFEAVENSTVCRCGSPGFRKNOGDEACTHCIPIN	300
QY	279	SRTTSEGATNCVCRNGYRRLADLDLDMECTTIPSAPOAVISVNETSLMLEMTPPRDSGC	338
Db	301	SRTTSEGATNCVCRNGYRRLADLDLDMECTTIPSAPOAVISVNETSLMLEMTPPRDSGC	360
QY	339	REDLYVNIITICKSCGSGRACITRCGDNVOYAPROLGLTEPRYISDLAHTQYTFEIOAVN	398
Db	361	REDLYVNIITICKSCGSGRACITRCGDNVOYAPROLGLTEPRYISDLAHTQYTFEIOAVN	420
QY	399	GWTDOSPSPFASVNITTTNOAASAVSIMQVSRVDSITLSWSQDPDPNGVILDELO	458
Db	421	GWTDOSPSPFASVNITTTNOAASAVSIMQVSRVDSITLSWSQDPDPNGVILDELO	480
QY	459	YXEKELSEYNATAIKSPNTVT	480
Db	481	YXEKELSEYNATAIKSPNTVT	502

RESULT 7  
HE-09-727

US-08-727-463-2  
; Sequence 2, Application US/08727463A

1 GENERAL INFORMATION:  
 2 APPLICANT: PAWSON, ANTHONY  
 3 APPLICANT: HENKEMEYER, MARK  
 4 APPLICANT: LETWIN, KENNETH  
 5 APPLICANT: MOUNT SINAI HOSPITAL CORPORATION  
 6 TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBSTANCES AFFECTING RECEPTOR  
 7 TITLE OF INVENTION: TYROSINE KINASE ACTIVITY (AS AMENDED)  
 8 FILE REFERENCE: 7933.89USMO  
 9 CURRENT APPLICATION NUMBER: US/08/727.463A  
 10 CURRENT FILING DATE: 1997-03-11  
 11 EARLIER APPLICATION NUMBER: PCT/CA95/00254  
 12 EARLIER FILING DATE: 1995-04-28  
 13 EARLIER APPLICATION NUMBER: 08/235.407  
 14 EARLIER FILING DATE: 1994-04-29

ORGANISM: Mus musculus  
US-08-727-463-2

Query Match	33.2%	Score 322	DB 11	Length 994
Best Local Similarity	100.0%	Pred. NO	0	
Matches 322	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

Qy 159 GFYLAIFODYGCMSSLAVRVFRKCPRIIINGAIFQETISGAESTSLVAARGSCINAAEE 218  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 181 GFYLAIFODYGCMSSLAVRVFRKCPRIIINGAIFQETISGAESTSLVAARGSCINAAEE 240

MOLECULE TYPE: peptide



```
Query Match          33.2%; Score 322; DB 11; Length 994;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 159 GFYLAFODYGGCSLAVRVYRKRCPRIIONGAIFQETLSGAEISTLVAAAGSCIANAE 218
      |||
Db 181 GFYLAFODYGGCSLAVRVYRKRCPRIIONGAIFQETLSGAEISTLVAAAGSCIANAE 240

OY 219 VDPVPIKLYCGDGEMLVPIRCMKAGFEAVENGTCRGCPSGEFKANOGEACTHCPIP 278
      |||
Db 241 VDPVPIKLYCGDGEMLVPIRCMKAGFEAVENGTCRGCPSGEFKANOGEACTHCPIP 300

OY 279 SRTSEGATNCVCHNGYRRADLPDLPCTTIPSAPOAVISVNETSLMEPTPRDSCG 338
      |||
Db 301 SRTSEGATNCVCHNGYRRADLPDLPCTTIPSAPOAVISVNETSLMEPTPRDSCG 360

OY 339 REDLVYNIICKSCGSGGACTRCGDNQVAPROLGLTEPRIYISDLAHQYTFEIOAVN 398
      |||
Db 361 REDLVYNIICKSCGSGGACTRCGDNQVAPROLGLTEPRIYISDLAHQYTFEIOAVN 420

OY 399 GVTQSPSPQFASVNTTNOAPSAVSIMHOVSRVDSITLSMSPDOPNGVILDYELQ 458
      |||
Db 421 GVTQSPSPQFASVNTTNOAPSAVSIMHOVSRVDSITLSMSPDOPNGVILDYELQ 480

OY 459 YEKELSEYNATAIKSPNTVT 480
      |||
Db 481 YEKELSEYNATAIKSPNTVT 502

RESULT 10
US-60-206-600-138
: Sequence 138, Application US/60206600
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
: TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
: FILE REFERENCE: CL000627
: CURRENT APPLICATION NUMBER: US/60/206,600
: CURRENT FILING DATE: 2000-05-31
: NUMBER OF SEQ ID NOS: 172
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 138
: LENGTH: 551
: TYPE: PRT
: ORGANISM: HUMAN
US-60-206-600-138

Query Match          20.4%; Score 198; DB 23; Length 551;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 574 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 633
      |||
Db 157 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 216

OY 634 VAIKTLKSGYTEKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMITTEFMENGSLDS 693
      |||
Db 217 VAIKTLKSGYTEKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMITTEFMENGSLDS 276

OY 694 FLRNDGQFTYIOLVGLRGIAAGMKYLA DMNVYHRDLAARNILVNSMLVCKVSDFGLSR 753
      |||
Db 277 FLRNDGQFTYIOLVGLRGIAAGMKYLA DMNVYHRDLAARNILVNSMLVCKVSDFGLSR 336

OY 754 FLEDDTSDPTYTSALGSK 771
      |||
Db 337 FLEDDTSDPTYTSALGSK 354

RESULT 11
US-60-208-965-196
```

```
: Sequence 196, Application US/60208965
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
: TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
: FILE REFERENCE: CL000639
: CURRENT APPLICATION NUMBER: US/60/208,965
: CURRENT FILING DATE: 2000-06-02
: NUMBER OF SEQ ID NOS: 244
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 196
: LENGTH: 551
: TYPE: PRT
: ORGANISM: HUMAN
US-60-208-965-196

Query Match          20.4%; Score 198; DB 23; Length 551;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 574 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 633
      |||
Db 157 TPQMKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKPGKREIF 216

OY 634 VAIKTLKSGYTEKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMITTEFMENGSLDS 693
      |||
Db 217 VAIKTLKSGYTEKORRDLSEASIMGQFDPHPNVHLEGVTKSTPVMITTEFMENGSLDS 276

OY 694 FLRNDGQFTYIOLVGLRGIAAGMKYLA DMNVYHRDLAARNILVNSMLVCKVSDFGLSR 753
      |||
Db 277 FLRNDGQFTYIOLVGLRGIAAGMKYLA DMNVYHRDLAARNILVNSMLVCKVSDFGLSR 336

OY 754 FLEDDTSDPTYTSALGSK 771
      |||
Db 337 FLEDDTSDPTYTSALGSK 354

RESULT 12
US-60-233-606-78
: Sequence 78, Application US/60233606
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
: TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
: FILE REFERENCE: CL000821
: CURRENT APPLICATION NUMBER: US/60/233,606
: CURRENT FILING DATE: 2000-09-18
: NUMBER OF SEQ ID NOS: 174
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 78
: LENGTH: 191
: TYPE: PRT
: ORGANISM: HUMAN
US-60-233-606-78

Query Match          11.4%; Score 111; DB 23; Length 191;
Best Local Similarity 100.0%; Pred. No. 4.9e-108;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 773 PIRMTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTQODVYNAIEQDYRLPP 832
      |||
Db 5 PIRMTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTQODVYNAIEQDYRLPP 64

OY 833 MDCPSALHQLMLDCMOKDRNHRPKFGQIVNTLDMKIRPNLSLKAAAPLSSG 883
      |||
Db 65 MDCPSALHQLMLDCMOKDRNHRPKFGQIVNTLDMKIRPNLSLKAAAPLSSG 115

RESULT 13
```

```

US-60-248-798-295
; Sequence 295, Application US/60248798
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1000945
; CURRENT APPLICATION NUMBER: US/60/248,798
; CURRENT FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 552
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 162
; TYPE: PRT
; ORGANISM: human
US-60-248-798-295

```

```

Query Match      10.1%; Score 98; DB 23; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.2e-94;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 773 PIRMTAPEAIQYRKFTSASDVMSYGIYMEVMSYGERPYMDMTNODYINAIEDYRLPPP 832
DB 65 PIRMTAPEAIQYRKFTSASDVMSYGIYMEVMSYGERPYMDMTNODYINAIEDYRLPPP 124
QY 833 MDCPSALHQLMLDQWQDRNRHRRPFGQIVNTLDMKIRN 870
DB 125 MDCPSALHQLMLDQWQDRNRHRRPFGQIVNTLDMKIRN 162

```

```

RESULT 14
US-60-160-202-4014
; Sequence 4014, Application US/60160202
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; FILE REFERENCE: C1000114
; CURRENT APPLICATION NUMBER: US/60/160,202
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4392
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4014
; LENGTH: 84
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-202-4014

```

```

Query Match      8.6%; Score 83; DB 23; Length 84;
Best Local Similarity 100.0%; Pred. No. 8.1e-79;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 614 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLSEASIMGQFDPNVIHLEGVY 673
DB 2 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLSEASIMGQFDPNVIHLEGVY 61
QY 674 TKSTPVMITTEFMENGLSDSFLR 696
DB 62 TKSTPVMITTEFMENGLSDSFLR 84

```

```

RESULT 15
US-60-160-209-3995
; Sequence 3995, Application US/60160209
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS AND USES
; FILE REFERENCE: C1000113

```

```

; CURRENT APPLICATION NUMBER: US/60/160,209
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4646
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3995
; LENGTH: 94
; TYPE: PRT
; ORGANISM: HUMAN
US-60-160-209-3995

```

```

Query Match      8.6%; Score 83; DB 23; Length 94;
Best Local Similarity 100.0%; Pred. No. 9e-79;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 614 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLSEASIMGQFDPNVIHLEGVY 673
DB 2 GEGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORRDFLSEASIMGQFDPNVIHLEGVY 61
QY 674 TKSTPVMITTEFMENGLSDSFLR 696
DB 62 TKSTPVMITTEFMENGLSDSFLR 84

```

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Search completed: July 24, 2001, 16:34:52
Job time: 153 sec

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Wed Jul 25 13:03:51 2001

us-09-378-759-11.oli.rapm

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```

Db      361 CGDNVOYAPRQLGLEPRRIYISDLAHTQYFETIOAVNGVTJDSPSPQFASVNTITNOA 420
QY      421 APSASIMHOVSRTVDSTLTSKSGPDQPNGLIDLEYELQYKEKELSENNATAIKSPITVT 480
      |||||||
Db      421 APSASIMHOVSRTVDSTLTSKSGPDQPNGLIDLEYELQYKEKELSENNATAIKSPITVT 480
QY      481 GLKAGAIYFQVRRATYAGYGRYSGKMYFQMTAEAYQTSIOEFLPLITISSAAGLVELI 540
      |||||||
Db      481 GLKAGAIYFQVRRATYAGYGRYSGKMYFQMTAEAYQTSIOEFLPLITISSAAGLVELI 540
QY      541 ANVYIAIVCNKRGFERADSEYTDKLOHTYSGHTPGMKIYIDPPTYEDPNEAVEFEAKEI 600
      |||||||
Db      541 ANVYIAIVCNKRGFERADSEYTDKLOHTYSGHTPGMKIYIDPPTYEDPNEAVEFEAKEI 600
QY      601 DISCVKLEOYIAGGEFEGVSGHKLPGKREIFAITKLKSGYERKRRRPFSLASIMGO 660
      |||||||
Db      601 DISCVKLEOYIAGGEFEGVSGHKLPGKREIFAITKLKSGYERKRRRPFSLASIMGO 660
QY      661 FDHPNVTHLEGVYTKSTPVMITTEFMENGSLDSFLRONDGQFTYIOLVGMRLGTAAGMKY 720
      |||||||
Db      661 FDHPNVTHLEGVYTKSTPVMITTEFMENGSLDSFLRONDGQFTYIOLVGMRLGTAAGMKY 720
QY      721 LADPNVYHRDLAARNILVNSNLCKVSDPGLSRPLEDDTSDPTYTSALGSKFPIRTWTAPE 780
      |||||||
Db      721 LADPNVYHRDLAARNILVNSNLCKVSDPGLSRPLEDDTSDPTYTSALGSKFPIRTWTAPE 780
QY      781 AIQYRKFTSASDVMSYGIWMMEVMSYGERPYMDTNDVINAIEODVRLPPMDCPALH 840
      |||||||
Db      781 AIQYRKFTSASDVMSYGIWMMEVMSYGERPYMDTNDVINAIEODVRLPPMDCPALH 840
QY      841 QLMIDCQKQRNHRPKFGQIVNTLDMKIRNPNLSIKAMAPLSSGINTPLDRTIPDYTSFN 900
      |||||||
Db      841 QLMIDCQKQRNHRPKFGQIVNTLDMKIRNPNLSIKAMAPLSSGINTPLDRTIPDYTSFN 900
QY      901 TYDEMLAIFMGQYKSEFANAGTSPVVSOMMEDILRVGVLAGHOKILNSIOVMRA 960
      |||||||
Db      901 TYDEMLAIFMGQYKSEFANAGTSPVVSOMMEDILRVGVLAGHOKILNSIOVMRA 960
QY      961 QMNQIOSVEV 970
      |||||||
Db      961 QMNQIOSVEV 970
      |||||||

RESULT 2
148760
protein-tyrosine kinase (EC 2.7.1.112) sek-3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Feb-2000
C:Accession: I48760; S42846
R:Becker, N.; Seltanidou, T.; Murphy, P.; Mattei, M.G.; Topilko, P.; Nieto, M.A.; Wilkitt
Mech. Dev. 47, 3-17, 1994
A:Title: Several receptor tyrosine kinase genes of the Eph family are segmentally expres
A:Reference number: I48759; MUID:95034306
A:Accession: I48760
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-480 <RES>
A:Cross-references: EMBL:X76011; NID:g4460055; PIDN:CAAS3598.1; PID:g4460056
C:Genetics:
A:Gene: Sek-3
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein k
F:121-129/Domain: protein kinase homology <KIN>
F:121-129/Region: protein kinase ATP-binding motif
F:404-470/Domain: SAM homology <SAM>

Query Match      30.5%; Score 296; DB 2; Length 480;
Best Local Similarity 99.7%; Pred. No. 1.4e-296;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPPTYEDPNEAVEFEAKELDISCVKLEOYIAGGEFEGVSGHKLPGKREIF 633
      |||||||

```

```

Db      84 TPGMKIYIDPPTYEDPNEAVEFEAKELDISCVKLEOYIAGGEFEGVSGHKLPGKREIF 143
QY      634 VAIKTKSGYTERKQRNDELSEASIMGOFDHPNVIHLEGVTKSTPVMITTEFMENGSLDS 693
      |||||||
Db      144 VAIKTKSGYTERKQRNDELSEASIMGOFDHPNVIHLEGVTKSTPVMITTEFMENGSLDS 203
QY      694 FLNONGQFTVIOVGMRLGTAAGMKYLDAMNVVHDLAARNILVNSNLCKVSDPGLSLR 753
      |||||||
Db      204 FLNONGQFTVIOVGMRLGTAAGMKYLDAMNVVHDLAARNILVNSNLCKVSDPGLSLR 263
QY      754 FLEDDTSDPTYTSALGSKFPIRTWTAPEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYMD 813
      |||||||
Db      264 FLEDDTSDPTYTSALGSKFPIRTWTAPEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYMD 323
QY      814 MTNODVINAIEODVFLPPMDCPALHQLMIDCQKQRNHRPKFGQIVNTLDMKIRNPNLS 873
      |||||||
Db      324 MTNODVINAIEODVFLPPMDCPALHQLMIDCQKQRNHRPKFGQIVNTLDMKIRNPNLS 383
QY      874 LKMAAPLSSGINTPLDRTIPDYTSFNPTDENTLEAIKMGQYKSEFANAGTSPDVVSOMK 933
      |||||||
Db      384 LKMAAPLSSGINTPLDRTIPDYTSFNPTDENTLEAIKMGQYKSEFANAGTSPDVVSOMK 443
QY      934 MEDILRVGVTLAGHCKKILNSIOVMRAQMNQIOSVEV 970
      |||||||
Db      444 MEDILRVGVTLAGHCKKILNSIOVMRAQMNQIOSVEV 480
      |||||||

RESULT 3
A57174
protein-tyrosine kinase (EC 2.7.1.112) erk - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000
C:Accession: A57174; S23362; S40294; PM0547
R:Salto, T.; Seki, N.; Matsuda, Y.; Kitahara, M.; Murata, M.; Kanda, N.; Nomura, N.;
Genomics 26, 382-384, 1995
A:Title: Identification of the human ERK gene as a putative receptor tyrosine kinase
A:Reference number: A57174; MUID:95324932
A:Accession: A57174
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-478 <SAL>
A:Cross-references: GB:D37827; NID:g1060894; PIDN:BAAO7073.1; PID:g1060895
R:Chan, J.; Watt, V.M.
Oncogene 6, 1057-1061, 1991
A:Title: eek and erk, new members of the eph subclass of receptor protein-tyrosine ki
A:Reference number: S23362; MUID:91296384
A:Accession: S23362
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 144-154, 'N', 156-204 <CHA>
A:Cross-references: EMBL:X59292
R:Watt, V.M.
submitted to the EMBL Data Library, May 1991
A:Reference number: S40294
A:Accession: S40294
A:Molecule type: mRNA
A:Residues: 144-204 <WAT>
A:Cross-references: EMBL:X59292; NID:g31222; PIDN:CA41981.1; PID:g31223
R:Iwase, T.; Tanaka, M.; Suzuki, M.; Naito, Y.; Sugimura, H.; Kino, T.
Biochem. Biophys. Res. Commun. 194, 698-705, 1993
A:Title: Identification of protein-tyrosine kinase genes preferentially expressed in
A:Reference number: PM0547; MUID:93343925
A:Accession: PM0547
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 132-162, 'R', 154-478, 'X' <IWA>
A:Cross-references: DDBJ:D14717
C:Genetics:
A:Gene: GDB:ERK
A:Cross-references: GDB:128637; OMIM:176946
A:Map position: IP36.1-IP36.1
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein

```

F:111-379/Domain: protein kinase homology <KIN>  
 F:119-127/Region: protein kinase ATP-binding motif  
 F:402-468/Domain: SAM homology <SAM>

Query Match 20.4%; Score 198; DB 2; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-195;  
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPQKKIYIDPFTYEDPNEAVREFAKEIDISCVKIEOVIGAGEGEGVCSGHLKPKREIF 633  
 |||||||  
 Db 82 TPQKKIYIDPFTYEDPNEAVREFAKEIDISCVKIEOVIGAGEGEGVCSGHLKPKREIF 141  
 |||||||  
 QY 634 VAITLKSQYTERKORRDLSEASIMGQFDPNPVTHLEGVTKSPVWITTEFMENGSLDS 693  
 |||||||  
 Db 142 VAITLKSQYTERKORRDLSEASIMGQFDPNPVTHLEGVTKSPVWITTEFMENGSLDS 201  
 |||||||  
 QY 694 FLRNDGQFTYIOLVGMIRGIAAGKTYLADNMVYHRLAARNILVNSLVCKVSDFGLSR 753  
 |||||||  
 Db 202 FLRNDGQFTYIOLVGMIRGIAAGKTYLADNMVYHRLAARNILVNSLVCKVSDFGLSR 261  
 |||||||  
 QY 754 FLEDDTSDPPTYTSALGCK 771  
 |||||||  
 Db 262 FLEDDTSDPPTYTSALGCK 279  
 |||||||

RESULT 4  
 A:Accession: A56599  
 embryo kinase 5 - chicken  
 N:Alternate names: receptor tyrosine kinase Cdk5  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 04-Feb-2000  
 C:Accession: A56599  
 R:Pasquale, E.B.  
 Cell Regul. 2, 523-534, 1991  
 A:Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor  
 A:Reference number: A56599; MUID:92144672  
 A:Accession: A56599  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-995 <PAS>  
 A:Cross-references: GB:M62325; NID:q211448; PIDN:AAA8667.1; PID:q211449  
 A:Note: sequence extracted from NCBI backbone (NCIN:81999, NCBI:P82001)  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein K1  
 F:628-996/Domain: protein kinase homology <KIN>  
 F:636-644/Region: protein kinase ATP-binding motif  
 F:919-985/Domain: SAM homology <SAM>

Query Match 10.6%; Score 103; DB 2; Length 995;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-97;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPQKKIYIDPFTYEDPNEAVREFAKEIDISCVKIEOVIGAGEGEGVCSGHLKPKREIF 633  
 |||||||  
 Db 599 TPQKKIYIDPFTYEDPNEAVREFAKEIDISCVKIEOVIGAGEGEGVCSGHLKPKREIF 658  
 |||||||  
 QY 634 VAITLKSQYTERKORRDLSEASIMGQFDPNPVTHLEGVTKS 676  
 |||||||  
 Db 659 VAITLKSQYTERKORRDLSEASIMGQFDPNPVTHLEGVTKS 701  
 |||||||

RESULT 5  
 A:Accession: A24910  
 probable tyrosine kinase R11 - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-May-1998  
 C:Accession: A24910  
 R:Posner, D.A.; Levy, J.B.; Daley, G.Q.; Simon, M.C.; Hanafusa, H.  
 Mol. Cell. Biol. 6, 325-331, 1986  
 A:Title: Isolation of chicken cellular DNA sequences with homology to the region of v-src

A:Reference number: A93080; MUID:87064304  
 A:Accession: A24910  
 A:Molecule type: DNA  
 A:Residues: 1-84 <POS>  
 A:Note: It is not known whether this gene is expressed  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; transmembrane protein  
 F:1-84/Domain: protein kinase homology (fragment) <KIN>

Query Match 5.1%; Score 49; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-42;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 720 YLADNMVYHRLAARNILVNSLVCKVSDFGLSRPLEDDTSDPPTYTSAL 768  
 |||||||  
 Db 13 YLADNMVYHRLAARNILVNSLVCKVSDFGLSRPLEDDTSDPPTYTSAL 61  
 |||||||

RESULT 6  
 JC5672  
 receptor tyrosine kinase (EC 2.7.-.-) Etk precursor - mouse  
 N:Alternate names: developmental kinase 1  
 C:Species: Mus musculus (house mouse)  
 C>Date: 20-Nov-1997 #sequence\_revision 20-Nov-1997 #text\_change 18-Jun-1999  
 C:Accession: JC5672; 148611; S51740  
 R:Talukder, A.H.; Muramatsu, T.; Kaneda, N.  
 Cell Struct. Funct. 22, 477-485, 1997  
 A:Title: A novel truncated variant form of Etk/MDK1 receptor tyrosine kinase is expressed  
 A:Reference number: JC5672; MUID:98035156  
 A:Accession: JC5672  
 A:Molecule type: mRNA  
 A:Residues: 1-998 <TAL>  
 A:Experimental source: embryo  
 R:Closek, T.; Millaer, B.; Ullrich, A.  
 Oncogene 9, 97-108, 1995  
 A:Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a n  
 A:Reference number: 148611  
 A:Accession: 148611  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-998 <RES>  
 A:Cross-references: EMBL:X79082; NID:9607133; PIDN:CAAS5687.1; PID:9607134  
 C:Comment: This enzyme plays a role during development involving differentiation and  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; brain; phosphotransferase; transmembrane protein  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-698/Product: receptor tyrosine kinase Etk #status predicted <MAT>  
 F:31-553/Domain: extracellular #status predicted <EXT>  
 F:331-438/Domain: fibronectin type III repeat <FN1>  
 F:441-534/Domain: fibronectin type III repeat <FN2>  
 F:554-579/Domain: transmembrane #status predicted <TM>  
 F:631-897/Domain: protein kinase homology <KIN>  
 F:639-647/Region: protein kinase ATP-binding motif  
 F:920-986/Domain: SAM homology <SAM>

Query Match 4.1%; Score 40; DB 2; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 3e-32;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 RWTAPAIQYRKFTSASDYWSGYWMEVSYGERPYWDM 814  
 |||||||  
 Db 801 RWTAPAIQYRKFTSASDYWSGYWMEVSYGERPYWDM 840  
 |||||||

RESULT 7  
 158351  
 receptor protein-tyrosine kinase - human  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
 C:Accession: 158351  
 R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch

Oncogene 10, 897-905, 1995  
 A:Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty  
 A:Reference number: 158351; MUID:95206782  
 A:Accession: 158351  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-998 <RES>  
 A:Cross-references: GB:136642; NID:9551607; PIDN:AAA74243.1; PID:9551608  
 C:Genetics:  
 A:Gene: HEK11  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; transmembrane protein  
 F:631-897/Domain: protein kinase homology <KIN>  
 F:639-647/Region: protein kinase ATP-binding motif  
 F:920-986/Domain: SAM homology <SAM>

Query Match 4.1%; Score 40; DB 2; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 3e-32;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RWTAPAIQYRKFTSADVSYGVMEVMSYGERPYDM 814  
 |||  
 DB 801 RWTAPAIQYRKFTSADVSYGVMEVMSYGERPYDM 840

RESULT 8  
 PT0187  
 protein-tyrosine kinase (EC 2.7.1.112) tyro-5 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 04-Feb-2000  
 C:Accession: PT0187  
 R:Li, C.; Lemke, G.  
 Neuron 6, 691-704, 1991  
 A:Title: An extended family of protein-tyrosine kinase genes differentially expressed in  
 A:Reference number: PT0183; MUID:91222560  
 A:Accession: PT0187  
 A:Molecule type: mRNA  
 A:Residues: 1-57 <LAI>  
 A:Experimental source: sciatic nerve  
 C:Genetics:  
 A:Gene: tyro-5  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki  
 F:1-57/Domain: protein kinase homology (fragment) <KIN>

Query Match 3.8%; Score 37; DB 2; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 NIIVNSMLVCKVSDFGISRPLEDDTSDPYTSALGK 771  
 |||  
 DB 1 NIIVNSMLVCKVSDFGISRPLEDDTSDPYTSALGK 37

RESULT 9  
 S33506  
 protein-tyrosine kinase (EC 2.7.1.112) Cdk9 - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 04-Feb-2000  
 C:Accession: S33506  
 R:Sajjadi, F.G.; Pasquale, E.B.  
 submitted to the EMBL Data Library, December 1992  
 A:Description: Five additional avian Eph-related tyrosine kinases are differentially exp  
 A:Reference number: S33502  
 A:Accession: S33506  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-612 <SAJ>  
 A:Cross-references: EMBL:219060  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki

F:63-147/Domain: fibronectin type III repeat homology <3FR>  
 F:245-513/Domain: protein kinase homology <KIN>  
 F:253-261/Region: protein kinase ATP-binding motif  
 F:536-602/Domain: SAM homology <SAM>

Query Match 3.7%; Score 36; DB 2; Length 612;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-28;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 723 DMNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 758  
 |||  
 DB 365 DMNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 400

RESULT 10  
 I48761  
 protein-tyrosine kinase (EC 2.7.1.112) sek-4 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 04-Feb-2000  
 C:Accession: I48761; S42847  
 R:Becker, N.; Seitanidou, T.; Murphy, P.; Mattei, M.G.; Topilko, P.; Nieto, M.A.; Wll  
 Mech. Dev. 47, 3-17, 1994  
 A:Title: Several receptor tyrosine kinase genes of the Eph family are segmentally exp  
 A:Reference number: I48759; MUID:95034306  
 A:Accession: I48761  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-275 <BEK>  
 A:Cross-references: EMBL:X76012; NID:9460057; PIDN:CA53599.1; PID:9460058  
 C:Genetics:  
 A:Gene: sek-4  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea  
 C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein  
 F:1-176/Domain: protein kinase homology (fragment) <KIN>  
 F:199-265/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-27;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 758  
 |||  
 DB 29 MNVHRDLAARNILVNSMLVCKVSDFGISRPLEDD 63

RESULT 11  
 I49071  
 protein kinase - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
 C:Accession: I49071  
 R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.  
 Mech. Dev. 48, 153-164, 1994  
 A:Title: Identification of novel protein kinases expressed in the myocardium of the d  
 A:Reference number: I49071; MUID:95200798  
 A:Accession: I49071  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-938 <RES>  
 A:Cross-references: EMBL:011493; NID:9595418; PIDN:AAA67925.1; PID:9595419  
 C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea  
 C:Keywords: ATP; transmembrane protein  
 F:571-839/Domain: protein kinase homology <KIN>  
 F:579-587/Region: protein kinase ATP-binding motif  
 F:862-928/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 938;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-27;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758  
DB 692 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 726

## RESULT 12

150611  
protein-tyrosine kinase (EC 2.7.1.112) Cdk10 - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 04-Feb-2000  
C:Accession: 150611; S33502  
R:Sajjadi, F.G.; Pasquale, E.B.  
Oncogene 8, 1807-1813, 1993  
A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.  
A:Reference number: 150611; MUID:93288394  
A:Accession: 150611  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-988 <SAS>  
A:Cross-references: EMBL:Z19061; NID:g312201; PIDN:CAA79511.1; PID:g312202  
C:Genetics:  
A:Gene: Cdk10  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein K1  
F:621-889/Domain: protein kinase homology <KIN>  
F:628-637/Region: protein kinase ATP-binding motif  
F:912-978/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 988;  
Best Local Similarity 100.0%; Pred. No. 4.3e-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758  
DB 742 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 776

## RESULT 13

148653  
mouse developmental kinase 5 (MDK5) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
C:Accession: 148653  
R:Ciossek, T.; Ierch, M.M.; Ullrich, A.  
Oncogene 11, 2085-2095, 1995  
A:Title: Cloning, characterization, and differential expression of MDK2 and MDK5, two novel human tyrosine kinases.  
A:Reference number: 148652; MUID:96074837  
A:Accession: 148653  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-993 <RES>  
A:Cross-references: EMBL:Z49086; NID:g1089899; PIDN:CAA88910.1; PID:g1089900  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
C:Keywords: ATP; transmembrane protein  
F:626-894/Domain: protein kinase homology <KIN>  
F:634-642/Region: protein kinase ATP-binding motif  
F:917-983/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 993;  
Best Local Similarity 100.0%; Pred. No. 4.3e-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758  
DB 747 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 781

## RESULT 14

S37627  
protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human  
C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 04-Feb-2000  
C:Accession: S37627  
R:Bohme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Streibhardt, K.; Ru  
Oncogene 8, 2857-2862, 1993  
A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.  
A:Reference number: S37627; MUID:93390963  
A:Accession: S37627  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-998 <BOE>

A:Cross-references: EMBL:X75208; NID:g406867; PIDN:CAA53021.1; PID:g406868  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein  
F:631-699/Domain: protein kinase homology <KIN>  
F:639-647/Region: protein kinase ATP-binding motif  
F:922-988/Domain: SAM homology <SAM>

Query Match 3.6%; Score 35; DB 2; Length 998;  
Best Local Similarity 100.0%; Pred. No. 4.3e-27;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 758  
DB 752 MNVYHDLAARNILVNSLVCKVSDFGLSRPLEDD 786

## RESULT 15

150612  
protein-tyrosine kinase (EC 2.7.1.112) Cdk6 - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 04-Feb-2000  
C:Accession: 150612; S33503  
R:Sajjadi, F.G.; Pasquale, E.B.  
Oncogene 8, 1807-1813, 1993  
A:Title: Five novel avian Eph-related tyrosine kinases are differentially expressed.  
A:Reference number: 150611; MUID:93288394  
A:Accession: 150612  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-952 <SAS>  
A:Cross-references: EMBL:Z19110; NID:g312901; PIDN:CAA79526.1; PID:g312902  
C:Genetics:  
A:Gene: Cdk6  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein  
F:585-853/Domain: protein kinase homology <KIN>  
F:593-601/Region: protein kinase ATP-binding motif  
F:876-942/Domain: SAM homology <SAM>

Query Match 3.3%; Score 32; DB 2; Length 952;  
Best Local Similarity 100.0%; Pred. No. 5.2e-24;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 LDSFLRNDGQFTVIQVLGMLRGIAAGMKYLA 722  
DB 673 LDSFLRNDGQFTVIQVLGMLRGIAAGMKYLA 704

Search completed: July 24, 2001, 16:33:51  
Job time: 137 sec



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## OM protein - protein search, using sw model

Run on: July 24, 2001, 16:33:29 ; Search time 14.77 Seconds

(without alignments)  
2249.683 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 970  
Sequence: 1 LIAAVEETLMOSTTATFELG.....IINSTQVRAQNMQIQSEV 970

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Swissprot\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	57.4	1055	EPB2_HUMAN	P29323 homo sapien
2	322	33.2	993	EPB2_MOUSE	P54756 mus musculu
3	103	10.6	987	EPB2_COTJA	Q90344 coturnix co
4	103	10.6	1004	EPB2_CHICK	P28693 gallus gall
5	40	4.1	993	EPB7_CHICK	Q42422 gallus gall
6	40	4.1	998	EPB7_HUMAN	Q5375 homo sapien
7	40	4.1	998	EPB7_MOUSE	Q61772 mus musculu
8	40	4.1	998	EPB7_RAT	P54759 rattus norv
9	36	3.7	1002	EPB5_CHICK	Q07457 gallus gall
10	35	3.6	988	EPB3_CHICK	Q07458 gallus gall
11	35	3.6	993	EPB3_MOUSE	P54754 mus musculu
12	35	3.6	998	EPB3_HUMAN	P54753 homo sapien
13	33	3.4	974	EPB3_XENLA	Q01735 xenopus lae
14	32	3.3	984	EPB1_CHICK	Q07454 gallus gall
15	32	3.3	984	EPB1_HUMAN	P54752 homo sapien
16	31	3.2	992	EPB4_XENLA	Q13148 brachydanio
17	31	3.2	902	EPB8_XENLA	Q01736 xenopus lae
18	31	3.2	984	EPB1_RAT	P09759 rattus norv
19	31	3.2	985	EPB4_XENLA	Q01571 xenopus lae
20	31	3.2	985	EPB4_XENLA	Q01845 xenopus lae
21	31	3.2	986	EPB4_XENLA	Q01845 xenopus lae
22	31	3.2	986	EPB4_CHICK	Q07456 gallus gall
23	31	3.2	986	EPB4_HUMAN	P54764 homo sapien
24	31	3.2	986	EPB4_MOUSE	Q03137 mus musculu
25	31	3.2	987	EPB4_HUMAN	P54760 homo sapien
26	31	3.2	987	EPB4_MOUSE	P54761 mus musculu
27	30	3.1	976	EPB2_HUMAN	P29317 homo sapien
28	30	3.1	977	EPB2_MOUSE	Q03145 mus musculu
29	28	2.9	948	EPB6_RAT	P54758 rattus norv
30	28	2.9	1013	EPB5_CHICK	P54755 gallus gall
31	26	2.7	1035	EPB6_MOUSE	Q03241 mus musculu
32	26	2.7	500	EPB3_RARE	Q13147 brachydanio
33	24	2.5	877	EPB5_MOUSE	Q06029 mus musculu

## ALIGNMENTS

RESULT 1	EPB2_HUMAN	STANDARD;	PRT; 1055 AA.	
ID	EPB2_HUMAN			
AC	P29323; 043477;			
DT	01-DEC-1992 (Ref. 24, Created)			
DT	01-OCT-2000 (Ref. 40, Last sequence update)			
DT	01-OCT-2000 (Ref. 40, Last annotation update)			
DE	EPHRAIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-3) (DRT) (RECEPTOR PROTEIN-TYROSINE KINASE HEK5) (BRK).			
GN	EPH2 OR EPH3 OR ERK OR DRT OR HEK5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=96154673; PubMed=8598679;			
RA	Ikegaki N., Tang X.X., Lin X.-G., Biegel J.A., Allen C.,			
RA	Yoshida A., Sultan E.P., Brodeur G.M., Pleasure D.E.;			
RT	"Molecular characterization and chromosomal localization of DRT (EPH2): a developmentally regulated human protein-tyrosine kinase gene of the EPH family.";			
RT	Hum. Mol. Genet. 4:2033-2045(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).			
RC	TISSUE=Gastric carcinoma;			
RX	MEDLINE=93343925; PubMed=7688222;			
RA	Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;			
RT	"Identification of protein-tyrosine kinase genes preferentially expressed in embryo stomach and gastric cancer.";			
RT	Biochem. Biophys. Res. Commun. 194:698-705(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM).			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=98359217; PubMed=9696046;			
RA	Tang X.X., Pleasure D.E., Brodeur G.M., Ikegaki N.;			
RT	"A variant transcript encoding an isoform of the human protein tyrosine kinase EPH2 is generated by alternative splicing and alternative use of polyadenylation signals.";			
RT	Oncogene 17:521-526(1998).			
RN	[4]			
RP	SEQUENCE OF 15-986 FROM N.A. (SHORT ISOFORM).			
RC	TISSUE=Brain;			
RX	MEDLINE=95206782; PubMed=7898931;			
RA	Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,			
RA	Basu R., Welcher A.A.;			
RT	"cDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases.";			
RT	Oncogene 10:897-905(1995).			
RN	[5]			
RP	SEQUENCE OF 509-986 FROM N.A. (SHORT ISOFORM).			
RC	TISSUE=Brain;			
RA	Saito T., Nohiko S., Kishihara M., Murata M., Yamamoto Y.,			
RA	Hori T., Matsuda Y.;			

34	24	2.5	1005	1	EPB5_RAT	P54757 rattus norv
35	20	2.1	981	1	EPB3_RARE	Q13146 brachydanio
36	19	2.0	1037	1	EPB5_HUMAN	P54756 homo sapien
37	16	1.6	983	1	EPB3_MOUSE	P29320 homo sapien
38	16	1.6	983	1	EPB3_MOUSE	P29319 mus musculu
39	16	1.6	984	1	EPB3_RAT	Q08680 rattus norv
40	15	1.5	534	1	EPB1_MOUSE	Q06750 mus musculu
41	15	1.5	976	1	EPB1_HUMAN	P21709 homo sapien
42	15	1.5	983	1	EPB3_CHICK	P29318 gallus gall
43	15	1.5	1006	1	EPB6_HUMAN	Q15197 homo sapien
44	15	1.5	1014	1	EPB6_MOUSE	Q08644 mus musculu
45	12	1.2	372	1	EPB5_RAT	P29321 rattus norv

RL Submitted (AUG-1994) to the EMBL/Genbank/DBJ databases.  
 RN [6]  
 RX SEQUENCE OF 652-712 FROM N.A.  
 RA MEDLINE-91296384; PubMed-1648701;  
 RT Chan J., Walt V.M.;  
 RT "eek and erk, new members of the eph subclass of receptor protein-  
 RT tyrosine kinases";  
 RL Oncogene 6:1057-1061(1991).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (SHORT ISOFORM).  
 RA MEDLINE-99132419; PubMed-9933164;  
 RT Thamos C.D., Goodwill K.E., Bowle J.U.;  
 RT "Oligomeric structure of the human Ephb2 receptor SAM domain";  
 RL Science 283:833-836(1999).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. THE LIGAND-  
 CC ACTIVATED FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-  
 CC ACTIVATING PROTEIN (RASGAP) THROUGH ITS SH2 DOMAIN. RASGAP BINDS  
 CC EPHB2 THROUGH THE JUXTAMEMBRANE TYROSINES RESIDUES (BY  
 CC SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/EPHB2V (SHOWN HERE)  
 CC AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, KIDNEY, PLACENTA,  
 CC PANCREAS, LIVER AND SKELETAL MUSCLE. PREFERENTIALLY EXPRESSED IN  
 CC FETAL BRAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: L41939; AAA99310.1; -  
 CC EMBL: D31661; BAA06306.1; -  
 CC EMBL: AF025304; AAB94602.1; -  
 CC EMBL: D14717; BAA03537.1; -  
 CC EMBL: L36643; AAA74244.1; -  
 CC EMBL: D37827; BAA7073.1; -  
 CC EMBL: X59292; CAA1981.1; -  
 CC PDB: 1BAF; 16-FEB-99.  
 CC MIM: 600997; -  
 CC InterPro: IPR000561; -  
 CC InterPro: IPR000719; -  
 CC InterPro: IPR001090; -  
 CC InterPro: IPR001245; -  
 CC InterPro: IPR001426; -  
 CC InterPro: IPR001660; -  
 CC InterPro: IPR001777; -  
 CC Pfam: PF01404; EPH\_Lbd; 1.  
 CC Pfam: PF00536; SAM; 1.  
 CC Pfam: PF00041; fn3; 2.  
 CC Pfam: PF00069; kinase; 1.  
 CC PRINTS: PR00014; FNYPEIIT.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 CC PROSITE: PS00791; EGF\_2; UNKNOWN; 1.  
 CC TRANSFERASE: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 CC Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;  
 CC Alternative splicing; Repeat.  
 CC SIGNAL 1 18 POTENTIAL.  
 CC CHAIN 19 1055 EPHRIN TYPE-B RECEPTOR 2.

FT	DOMAIN	19	543	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	544	564	POTENTIAL.
FT	DOMAIN	565	1055	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	184	324	CYS-RICH.
FT	DOMAIN	325	418	FIBRONECTIN TYPE-III.
FT	DOMAIN	436	520	FIBRONECTIN TYPE-III.
FT	DOMAIN	621	884	PROTEIN KINASE.
FT	DOMAIN	911	986	SAM.
FT	SITE	984	986	PDZ-BINDING MOTIF (POTENTIAL) (IN SHORT ISOFORM).
FT	NP_BIND	627	635	ATP (BY SIMILARITY).
FT	BINDING	653	653	ATP (BY SIMILARITY).
FT	ACT_SITE	746	746	ATP (BY SIMILARITY).
FT	MOD_RES	596	596	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	602	602	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES	780	780	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	930	930	PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	CARBOHYD	265	265	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	428	428	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	482	482	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	986	986	G -> V (IN SHORT ISOFORM).
FT	VARSPLIC	987	1055	MISSING (IN SHORT ISOFORM).
FT	VARIANT	671	671	A -> R.
FT	CONFLICT	1	20	/FTID-VAR 004162.
FT	CONFLICT	154	154	MAIRRGALILLPLAAVE -> MVVPLALPVCTYA
FT	CONFLICT	476	476	(IN REF. 2).
FT	CONFLICT	532	532	G -> D (IN REF. 2).
FT	CONFLICT	495	496	K -> KQ (IN REF. 2).
FT	CONFLICT	568	568	E -> D (IN REF. 2).
FT	CONFLICT	589	589	MISSING (IN REF. 4).
FT	CONFLICT	788	788	R -> RR (IN REF. 1).
FT	CONFLICT	853	853	M -> I (IN REF. 4).
FT	CONFLICT	923	923	I -> F (IN REF. 4).
FT	CONFLICT	956	956	S -> A (IN REF. 2 AND 5).
FT	CONFLICT	958	958	E -> K (IN REF. 2 AND 5).
FT	CONFLICT	958	958	L -> V (IN REF. 3).
FT	CONFLICT	958	958	V -> L (IN REF. 1).
SO	SEQUENCE	1055 AA;	117506 MW;	DOAA2CCBECBDB8 CRC64;

Query Match 57.4%; Score 557; DB 1; Length 1055;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 937; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY	1	LLAAVEETLMDSTTFAELGMMVHPSSGMEVSGYDENNTTIRTYQVAVFPSSQNNMLR	60
DB	15	LLAAVEETLMDSTTFAELGMMVHPSSGMEVSGYDENNTTIRTYQVAVFPSSQNNMLR	74
QY	61	TKFIRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYEADPDSATKTFPPNMENP	120
DB	75	TKFIRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYEADPDSATKTFPPNMENP	134
QY	121	WKVVDITIAADESESCVDLGRVWKINTEVRSFGVRSRSGFYLAFODYGGCMLSIAVRVY	180
DB	135	WKVVDITIAADESESCVDLGRVWKINTEVRSFGVRSRSGFYLAFODYGGCMLSIAVRVY	194
QY	181	RKCPRIQNGAIFQETLSAESTSLVAARGSCIANEEDVDPKILYCNDSGMIWPIGRC	240
DB	195	RKCPRIQNGAIFQETLSAESTSLVAARGSCIANEEDVDPKILYCNDSGMIWPIGRC	254
QY	241	MCKAGEAVENGTVRCGCGSGTFKANQGDGACTHCHINSRTSEGTATNCVCRNGYRADL	300
DB	255	MCKAGEAVENGTVRCGCGSGTFKANQGDGACTHCHINSRTSEGTATNCVCRNGYRADL	314
QY	301	DLDMCCTTIPSPAPCAVVISVNETSLMLEWTPPRDSGGRDLVYNIICKSCGSGRACRTR	360
DB	315	DLDMCCTTIPSPAPCAVVISVNETSLMLEWTPPRDSGGRDLVYNIICKSCGSGRACRTR	374
QY	361	CGDNVOYARQGLHPRRIYISDLAHTQYTFEIQAVNVTVTQSPSPQFASVNTITNQA	420
DB	375	CGDNVOYARQGLHPRRIYISDLAHTQYTFEIQAVNVTVTQSPSPQFASVNTITNQA	434

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OY 421 APSAVSIMHOVSRVSTITISMSOPDOPNGVILDELOYEKEKELSEXNATAIKSPNTVT 480
DB 435 APSVASIMHOVSRVSTITISMSOPDOPNGVILDELOYEKEKELSEXNATAIKSPNTVT 494
OY 481 --GLKAGAIYVFOVRATVAGYRGSKMVFQMTAEVOTSTQEKLPILIGSSAGLVF 538
DB 495 VQGLKAGAIYVFOVRATVAGYRGSKMVFQMTAEVOTSTQEKLPILIGSSAGLVF 554
OY 539 LIAVVAIAVCNRRGFERADSEYTKLOHYTSGHITPGMKIYIDPPTYEDPNAVREFAK 598
DB 555 LIAVVAIAVCNRRGFERADSEYTKLOHYTSGHITPGMKIYIDPPTYEDPNAVREFAK 614
OY 599 EIDISCKIEOVIGAGEFEVCGHKLKQKREIFAIVATITLKSQYTERKORPFLSEASIM 658
DB 615 EIDISCKIEOVIGAGEFEVCGHKLKQKREIFAIVATITLKSQYTERKORPFLSEASIM 674
OY 659 GQPDHNVNHLSEGVTKSTPVMITTEFMENGSLDSFLRONDOGFYIOVLGMRGIAQM 718
DB 675 GQPDHNVNHLSEGVTKSTPVMITTEFMENGSLDSFLRONDOGFYIOVLGMRGIAQM 734
OY 719 KYIADNMYHRLAARNILVNSNLCKVSDFGLSREFLEDSDPTVTYALGKFPRIWTA 778
DB 735 KYIADNMYHRLAARNILVNSNLCKVSDFGLSREFLEDSDPTVTYALGKFPRIWTA 794
OY 779 PEAIQYRKFTSADSVSYGIVMMEVSYGERPYMTNDVYNAIEODYRLRPPMDCPSA 838
DB 795 PEAIQYRKFTSADSVSYGIVMMEVSYGERPYMTNDVYNAIEODYRLRPPMDCPSA 854
OY 839 LHOQLMDCQKDRNHRPKFGQIVNTLDKMRNPSLKAAPLSSGINSPLDRTTPDYS 898
DB 855 LHOQLMDCQKDRNHRPKFGQIVNTLDKMRNPSLKAAPLSSGINSPLDRTTPDYS 914
OY 899 FMTVDEMLEAIFMGQYKESFANAQTSDDVYSQMMEDILR 939
DB 915 FMTVDEMLEAIFMGQYKESFANAQTSDDVYSQMMEDILR 955

RESULT 2
EPH2_MOUSE STANDARD: PRT: 993 AA.
ID AC PS4763: Q62213:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EPH-3) (NFK) (SEK-3) (FRAGMENT).
GN EPHB2 OR EPH3 OR NUK OR SEK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Henkemeyer M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 515-993 FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=95034306; PubMed=7947319;
RA Becker N., Settinidou T., Murphy P., Mattel M.-G., Topilko P.,
RA Nieto A., Wilkinson D.G., Charney P., Gilardi P.;
RT "Several receptor tyrosine kinase genes of the Eph family are
RT segmentally expressed in the developing hindbrain.";
RL Mech. Dev. 47:3-17(1994).
RN [3]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wldeman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. CAN

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CC CC FUNCTION: IN ASPECTS OF RETINAL GANGLION CELL AXON GUIDANCE TO THE
CC CC OPTIC DISK EVEN LACKING ITS TYROSINE KINASE DOMAIN. THE LIGAND-
CC CC ACTIVATED FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-
CC CC ACTIVATING PROTEIN (RASGAP) THROUGH ITS SH2 DOMAIN. RASGAP BINDS
CC CC EPHB2 THROUGH THE JUXTAMEMBRANE TYROSINES RESIDUES (BY
CC CC SIMILARITY).
CC CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC CC PROTEIN TYROSINE PHOSPHATE.
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE DEVELOPING OUTER
CC CC RETINA.
CC CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC CC RECEPTOR SUBFAMILY.
CC CC -----
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: L25890; AAA72411.1; ALT_INIT.
CC CC DR EMBL: X76011; CA53598.1; -.
CC CC DR HSSP: P00523; 2PTK
CC CC DR MGD: MGI:99611; Ephb2.
CC CC DR InterPro: IPR000561; -.
CC CC DR InterPro: IPR000719; -.
CC CC DR InterPro: IPR001090; -.
CC CC DR InterPro: IPR001245; -.
CC CC DR InterPro: IPR001426; -.
CC CC DR InterPro: IPR001660; -.
CC CC DR InterPro: IPR001777; -.
CC CC DR Pfam: PF01404; Eph_Lbd; 1.
CC CC DR Pfam: PF00536; SAM; 1.
CC CC DR Pfam: PF00041; fn3; 2.
CC CC DR Pfam: PF00069; pkinase; 1.
CC CC DR PROSITE: PS00107; PROTEIN_KINASE_TYR; 1.
CC CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC CC DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC CC DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC CC DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
CC CC KM Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC CC KM Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC CC FT NON_TER 1 1
CC CC FT SIGNAL <1 25
CC CC FT CHAIN 26 993
CC CC FT DOMAIN 26 550
CC CC FT TRANSMEM 551 571
CC CC FT DOMAIN 572 993
CC CC FT DOMAIN 191 328
CC CC FT DOMAIN 329 438
CC CC FT DOMAIN 439 536
CC CC FT DOMAIN 628 891
CC CC FT SITE 918 993
CC CC FT NP_BIND 991 993
CC CC FT BINDING 634 642
CC CC FT ACT_SITE 660 660
CC CC FT MOD_RES 753 753
CC CC FT MOD_RES 603 603
CC CC FT MOD_RES 609 609
CC CC FT MOD_RES 787 787
CC CC FT MOD_RES 937 937
CC CC FT CARBOHYD 272 272
CC CC FT CARBOHYD 343 343
CC CC FT CARBOHYD 435 435
CC CC FT CARBOHYD 489 489
CC CC FT CONFLICT 575 575
CC CC SEQUENCE 993 AA; 110628 MW; A0E1A695F46587E8 CRC64;

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Query Match      33.2%; Score 322; DB 1; Length 993;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 GFYLAPODYGGCSLAVRVYRKRPRRIQNGAIFQETLSGAESTSLVARGSCINAE 218
    |||||||
DB 180 GFYLAPODYGGCSLAVRVYRKRPRRIQNGAIFQETLSGAESTSLVARGSCINAE 239

QY 219 VDPPIKLYCGDEMLVPIGRCKMCKAGFEVNGTCRGCPSTFRANODECTCPIN 278
    |||||||
DB 240 VDPPIKLYCGDEMLVPIGRCKMCKAGFEVNGTCRGCPSTFRANODECTCPIN 299

QY 279 SRTSEGATNCVCRNGYRRADLPDLPCTTIPSAQAVISSVNETSLMLEWTPRDSG 338
    |||||||
DB 300 SRTSEGATNCVCRNGYRRADLPDLPCTTIPSAQAVISSVNETSLMLEWTPRDSG 359

QY 339 REDLVYNIICKSGSGRGACTRCGDNVQYAPRQLGLEPRITYSDLAHTQYTFEIOAVN 398
    |||||||
DB 360 REDLVYNIICKSGSGRGACTRCGDNVQYAPRQLGLEPRITYSDLAHTQYTFEIOAVN 419

QY 399 GYWDOSPFSPQFASVNTTNOAAPSAVSIMHOYSRTVDSITLSMSPDPQNGVILDELO 458
    |||||||
DB 420 GYWDOSPFSPQFASVNTTNOAAPSAVSIMHOYSRTVDSITLSMSPDPQNGVILDELO 479

QY 459 YEKELSEYNATAIKSPNTVT 480
    |||||||
DB 480 YEKELSEYNATAIKSPNTVT 501

RESULT 3
ID EPB2_COTJA STANDARD; PRT; 987 AA.
AC 090344;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR QEK5).
GN EPHB2 OR QEK5.
OS Ccuturix coturix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Cuculidae.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=96109331; PubMed=8612986;
RA Kenny D., Bronner-Fraser M., Marcelle C.;
RT "The receptor tyrosine kinase QEK5 mRNA is expressed in a gradient
RT within the neural retina and the tectum.";
RL Dev. Biol. 172:708-716(1995).
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X9137; CA62862.1; -
CC HSSP: P00523; 2PKK.
CC InterPro: IPR000561; -

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DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam: PF01404; EPH_1bd, 1.
DR Pfam: PF00536; SAM, 1.
DR Pfam: PF00041; In3, 2.
DR Pfam: PF00069; Kinase, 1.
DR PRINTS: PR00014; ENTYPETII.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN KINASE DOM. 1.
DR PROSITE: PS00109; PROTEIN KINASE ATP. 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM. 1.
DR PROSITE: PS00790; RECEPTOR_TIR_KIN_V.1, 1.
DR PROSITE: PS00791; RECEPTOR_TIR_KIN_V.2, 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 987
FT DOMAIN 20 544
FT TRANSMEM 545 565
FT DOMAIN 566 987
FT DOMAIN 185 332
FT DOMAIN 323 432
FT DOMAIN 433 510
FT DOMAIN 622 805
FT DOMAIN 912 987
FT SITE 985 987
FT NP_BIND 628 636
FT BINDING 654 654
FT ACT_SITE 747 747
FT MOD_RES 597 597
FT MOD_RES 603 603
FT MOD_RES 781 781
FT MOD_RES 931 931
FT CARBOHYD 266 266
FT CARBOHYD 337 337
FT CARBOHYD 429 429
FT CARBOHYD 478 478
FT CARBOHYD 483 483
FT SEQUENCE 987 AA; 110331 MW; 05D6ECC6B718DD7 CRC64;

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Query Match      10.6%; Score 103; DB 1; Length 987;
Best Local Similarity 100.0%; Pred. No. 1,le-102;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPGMKITIDPFTYEDPNEAVREFAKEIDISCVKIEBIVGAGEFEGVCSGHLKLPKREIF 633
    |||||||
DB 591 TPGMKITIDPFTYEDPNEAVREFAKEIDISCVKIEBIVGAGEFEGVCSGHLKLPKREIF 650

QY 634 VAIKTLKSGTEKORDFLSEASIMGOFHPNVIHLEGVTKS 676
    |||||||
DB 651 VAIKTLKSGTEKORDFLSEASIMGOFHPNVIHLEGVTKS 693

RESULT 4
ID EPB2_CHICK STANDARD; PRT; 1004 AA.
AC P28693;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR CEK5).
GN EPHB2 OR CEK5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

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NCBI\_TaxID=9031:

OX (1) SEQUENCE FROM N.A. (SHORT ISOFORM).

RP TISSUE-Embryo;

RC MEDLINE=92144672; PubMed=1664238;

RA Pasquale E.B.;

RT "identification of chicken embryo kinase 5, a developmentally regulated receptor-type tyrosine kinase of the Eph family.";

RL Cell Regul. 2:523-534(1991).

RL [2]

RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).

RC TISSUE-Brain;

RX MEDLINE=93288394; PubMed=8510926;

RA Sajiati F.G., Pasquale E.B.;

RT "Five novel avian Eph-related tyrosine kinases are differentially expressed.";

RL Oncogene 8:1807-1813(1993).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/CEK5+ (SHOWN HERE) AND A SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT DEVELOPMENT AND SUSTAINED EXPRESSION IN ADULT BRAIN. THE LONGER FORM (CEK5+) IS SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS SYSTEM.

CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.

-----

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CC -----

DR HSSP; M62325; AAA48667.1; ALT\_INIT.

DR HSSP; P00523; 2PTR.

DR Interpro: IPR000561; -

DR Interpro: IPR000719; -

DR Interpro: IPR001090; -

DR Interpro: IPR001245; -

DR Interpro: IPR001426; -

DR Interpro: IPR001660; -

DR Interpro: IPR001777; -

DR Pfam: PF001404; Eph\_Ibd; 1.

DR Pfam: PF00536; SAM; 1.

DR Pfam: PF00041; fn3; 2.

DR Pfam: PF00069; pkinase; 1.

DR PRINTS: PRO0014; FNTYPEI11.

DR PRINTS: PRO0109; TYRKINASE.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.

DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.

DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.

KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing; Repeat.

FT CHAIN 1 19

FT SIGNAL 20 1004

FT DOMAIN 20 544

FT TRANSMEM 545 565

FT DOMAIN 566 1004

FT DOMAIN 20 321

FT DOMAIN 326 419

FT DOMAIN 437 521

FT SIGNAL 1 19

FT CHAIN 20 1004

FT DOMAIN 20 544

FT TRANSMEM 545 565

FT DOMAIN 566 1004

FT DOMAIN 20 321

FT DOMAIN 326 419

FT DOMAIN 437 521

FT DOMAIN 639 902

FT DOMAIN 929 1004

FT SITE 1002 1004

FT NE\_BIND 645 653

FT BINDING 671 671

FT ACT\_SITE 764 764

FT MOD\_RES 614 614

FT MOD\_RES 620 620

FT MOD\_RES 798 798

FT MOD\_RES 948 948

FT CARBOHYD 266 266

FT CARBOHYD 337 337

FT CARBOHYD 429 429

FT CARBOHYD 478 478

FT CARBOHYD 483 483

FT VARSPPLIC 591 606

SO SEQUENCE 1004 AA; 111963 MW; BD26213970ECC6ED CRC64;

Query Match 10.6%; Score 103; DB 1; Length 1004;

Best local Similarity 100.0%; Pred. No. 1.2e-102;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 574 TPQMKIYIDPFYEDPNEAVREFAKEDISCVKIEQVIGAGEGVCSSHLKPKRKREIF 633

DB 608 TPQMKIYIDPFYEDPNEAVREFAKEDISCVKIEQVIGAGEGVCSSHLKPKRKREIF 667

OY 634 VAITKLSGTEKORDPFLSEASIMGFDPNVIHLEGVVTS 676

DB 668 VAITKLSGTEKORDPFLSEASIMGFDPNVIHLEGVVTS 710

RESULT 5

EPAY7 CHICK STANDARD; PRT; 993 AA.

AC 042422;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEPHA7) (TYROSINE-PROTEIN KINASE RECEPTOR CEK11).

GN CEPHA7 OR CEK11.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Embryo;

RX MEDLINE=98092111; PubMed=9431814;

RA Araujo M., Nieto M.A.;

RT "The expression of chick EphA7 during segmentation of the central and peripheral nervous system.";

RL Mech. Dev. 68:173-177(1997).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN FAMILY.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM.

CC RESTRICTED TO PHOSOMERES 1 AND 2 IN THE DORSAL HORN AND ALL THE RHOMBOMERES IN THE HIND BRAIN DURING SEGMENTATION STAGES. LATER ON, A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST AND MOTOR AXONS THROUGH THE SCLEROTOMES.

CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.

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EMBL: Y14271; CAA74643.1; -  
HSP: P00523; 2PTK.  
InterPro: IPR000719; -  
InterPro: IPR001090; -  
InterPro: IPR001245; -  
InterPro: IPR001426; -  
InterPro: IPR001660; -  
InterPro: IPR001777; -  
Pfam: PF01404; EPH\_1bd; 1.  
Pfam: PF00536; SAM; 1.  
Pfam: PF00041; fn3; 2.  
Pfam: PF00069; pkinase; 1.  
PRINTS: PR00014; FNTYPEIII.  
PRINTS: PR00107; TYRKINASE.  
PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT SIGNAL 1 30  
FT CHAIN 1 993  
FT DOMAIN 31 551  
FT TRANSMEM 552 572  
FT DOMAIN 573 993  
FT DOMAIN 192 328  
FT DOMAIN 329 438  
FT DOMAIN 439 536  
FT DOMAIN 628 889  
FT DOMAIN 916 993  
FT SITE 991 993  
FT NP\_BIND 916 993  
FT DISULFID 634 642  
FT BINDING 74 109  
FT ACT\_SITE 753 753  
FT MOD\_RES 603 603  
FT MOD\_RES 609 609  
FT MOD\_RES 786 786  
FT MOD\_RES 935 935  
FT CARBOHYD 343 343  
FT CARBOHYD 410 410  
SQ SEQUENCE 993 AA; 11366 MW; EECF9603047606BD CRC64;

Query Match 4.1%; Score 40; DB 1; Length 993;  
Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RMTAPEALQYRKFTSADVMSTGYVMWVSYGPRPYWDM 814  
DB 796 RMTAPEALQYRKFTSADVMSTGYVMWVSYGPRPYWDM 835

RESULT 6  
EPA7\_HUMAN STANDARD; PRT; 998 AA.  
AC Q15375;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
DE KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3) (RECEPTOR PROTEIN-  
DE TYROSINE KINASE HEK1).  
GN EPHAY OR EHK3 OR HEK1.  
OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
CC NCBI\_TaxId=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=95206782; PubMed=7898931;  
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,  
RA Basu R., Welcher A.A.;  
RT "cdna cloning and tissue distribution of five human EPH-like receptor  
protein-tyrosine kinases";  
RL Oncogene 10:897-905(1995).  
CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.  
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +  
CC PROTEIN TYROSINE PHOSPHATE.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.  
CC -!- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
CC RECEPTOR SUBFAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: L36642; AAA74243.1; -  
HSP: P00523; 2PTK.  
MIM: 602190; -  
InterPro: IPR000561; -  
InterPro: IPR000719; -  
InterPro: IPR001090; -  
InterPro: IPR001245; -  
InterPro: IPR001426; -  
InterPro: IPR001660; -  
InterPro: IPR001777; -  
Pfam: PF01404; EPH\_1bd; 1.  
Pfam: PF00536; SAM; 1.  
Pfam: PF00041; fn3; 2.  
Pfam: PF00069; pkinase; 1.  
PRINTS: PR00014; FNTYPEIII.  
PRINTS: PR00107; TYRKINASE.  
PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT SIGNAL 1 24  
FT CHAIN 25 998  
FT DOMAIN 25 556  
FT TRANSMEM 557 572  
FT DOMAIN 578 998  
FT DOMAIN 192 328  
FT DOMAIN 329 438  
FT DOMAIN 439 536  
FT DOMAIN 628 889  
FT DOMAIN 916 993  
FT SITE 991 993  
FT NP\_BIND 916 993  
FT BINDING 74 109  
FT ACT\_SITE 753 753  
FT MOD\_RES 603 603  
FT MOD\_RES 609 609  
FT MOD\_RES 786 786  
FT MOD\_RES 935 935  
FT CARBOHYD 343 343  
FT CARBOHYD 410 410  
SQ SEQUENCE 993 AA; 11366 MW; EECF9603047606BD CRC64;



FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 998 AA: 112096 MW: 479B9CA0D2B06EB CRC64:

Query Match 4.18: Score 40; DB 1; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 1,9e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 814  
 ||||||||||||||||||||||||||||||||||||||||  
 DB 801 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 840

RESULT 7  
 EPAT\_MOUSE STANDARD: PRT; 998 AA.  
 AC 061772; 061773; 061774; 061505;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
 DE KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3) (EMBRYONIC BRAIN  
 DE KINASE) (EBK) (DEVELOPMENTAL KINASE 1) (MDK-1).  
 GN EPHA7 OR EHK3 OR EBK OR MDK1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RA MEDLINE=95124729; PubMed=7824284;  
 RA Closssek T., Millauner B., Ullrich A.;  
 RT "Identification of alternatively spliced mRNAs encoding variants of  
 RT MDK1, a novel receptor tyrosine kinase expressed in the murine  
 RT nervous system.";  
 RT Oncogene 10:97-108(1995).  
 RN [2]  
 RP SEQUENCE OF 431-998 FROM N.A. (ISOFORM MDK1).  
 RC TISSUE-Brain;  
 RA MEDLINE=96081374; PubMed=8541219;  
 RA Ellis J., Liu Q., Breilman M., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,  
 RA Fletcher F.A., Ziegler S.F., Rogers J.H.;  
 RT "Embryo brain kinase: a novel gene of the eph/erbA receptor tyrosine  
 RT kinase family.";  
 RT Mech. Dev. 52:319-341(1995).  
 RL -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.  
 CC CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: MDK1 (SHOWN HERE), MDK1-1, MDK1-  
 CC 2, MDK1-T1 AND MDK1-T2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO. IN ADULT,  
 CC EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X79082; CAAS5687.1; -;  
 DR EMBL; X79083; CAAS5688.1; -;  
 DR EMBL; X79084; CAAS5689.1; -;  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DR EMBL; X81466; CAAS7224.1; -;  
 DR HSP; P00523; 2PTR.  
 DR MSG; MG1:952376; Epha7.  
 DR InterPro: IPR000561; -;  
 DR InterPro: IPR000739; -;  
 DR InterPro: IPR001090; -;  
 DR InterPro: IPR001245; -;  
 DR InterPro: IPR001426; -;  
 DR InterPro: IPR001660; -;  
 DR InterPro: IPR001777; -;  
 DR Pfam: PR01404; EPH\_Lbd; 1.  
 DR Pfam: PF00536; SAM; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0014; FNTYPEIIT.  
 DR PRINTS: PRO0107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN; 1.  
 KW transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing.  
 FT SIGNAL 1 29  
 FT CHAIN 30 998  
 FT DOMAIN 30 556  
 FT TRANSMEM 557 577  
 FT DOMAIN 578 998  
 FT DOMAIN 192 328  
 FT DOMAIN 329 438  
 FT DOMAIN 439 536  
 FT DOMAIN 633 894  
 FT DOMAIN 921 998  
 FT SITE 996 998  
 FT NF\_BIND 639 647  
 FT BINDING 665 665  
 FT ACT\_SITE 758 758  
 FT MOD\_RES 608 608  
 FT MOD\_RES 614 614  
 FT MOD\_RES 791 791  
 FT MOD\_RES 940 940  
 FT CARBOHYD 64 64  
 FT CARBOHYD 343 343  
 FT CARBOHYD 410 410  
 FT CARBOHYD 540 544  
 FT VARSPPLIC 601 604  
 FT VARSPPLIC 601 610  
 FT VARSPPLIC 611 998  
 FT VARSPPLIC 600 626  
 FT VARSPPLIC 627 998  
 FT CONFLICT 480 480  
 SQ SEQUENCE 998 AA: 11874 MW: 81C553BE15AE2FA CRC64:

Query Match 4.18: Score 40; DB 1; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 1,9e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 814  
 ||||||||||||||||||||||||||||||||||||||||  
 DB 801 RWTAPFAIOTRKFTSASDVMSYGIWMVMSYGERPYWDM 840

RESULT 8  
 EPAT\_MOUSE STANDARD: PRT; 998 AA.  
 AC P54759;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

01-OCT-2000 (Rel. 40). Last annotation update)  
 DE EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
 KINASE RECEPTOR EHK-3) (EPH HOMOLOG KINASE-3).  
 GN EPHA7 OR EHK3 OR EHK-3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxId=10116;  
 RN [1]  
 RP MEDLINE:95249272; PubMed:7731712;  
 RA Valenzuela D.M., Rojas E., Griffiths J.A., Compton D.L., Gisser M.,  
 RA Ip N.Y., Goldfarb M., Yancopoulos G.D.;  
 RT "Identification of full-length and truncated forms of EHK-3, a novel  
 member of the Eph receptor tyrosine kinase family.";  
 RL Oncogene 10:1573-1580(1995).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A1, -A2, -A3, -A4 AND -A5.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC TRUNCATED ISOFORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE  
 CC TRUNCATED FORM LACKS THE KINASE DOMAIN. THE LONG FORM IS MORE  
 CC WIDELY EXPRESSED IN THE EMBRYO.  
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U21954; AAA86830.1; -  
 DR EMBL: U21955; AAA86831.1; -  
 DR HSSP: P00523; 2PTK.  
 DR InterPro: IPR000561; -  
 DR InterPro: IPR000719; -  
 DR InterPro: IPR001090; -  
 DR InterPro: IPR001245; -  
 DR InterPro: IPR001426; -  
 DR InterPro: IPR001660; -  
 DR InterPro: IPR001777; -  
 DR Pfam: PF01404; EPH\_1bd; 1.  
 DR Pfam: PF00536; SAM; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00014; FNTYPEITI.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN; 1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing;  
 FT SIGNAL 1 24  
 FT CHAIN 1 998  
 FT DOMAIN 25 556 EPHRIN TYPE-A RECEPTOR 7.  
 FT TRAMSMEM 557 577 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 578 998 POTENTIAL.  
 FT DOMAIN 192 328 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 329 438 CYS-RICH.  
 FT DOMAIN 439 536 FIBRONECTIN TYPE-III.  
 FT DOMAIN 633 894 FIBRONECTIN TYPE-III.  
 FT DOMAIN PROTEIN KINASE.

FT DOMAIN 921 998 SAM.  
 FT SITE 996 998 EPZ BINDING MOTIF (POTENTIAL).  
 FT NP\_BIND 639 647 ATP (BY SIMILARITY).  
 FT BINDING 665 665 ATP (BY SIMILARITY).  
 FT ACT\_SITE 758 758 BY SIMILARITY.  
 FT MOD\_RES 608 608 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 614 614 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 791 791 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 940 940 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 600 610 FPKPTKTYID -> SLVTNENHLSVL (IN TRUNCATED  
 FT ISOFORM).  
 SQ SEQUENCE 998 AA; 111953 MW; A7A82A698924876C CMC64;  
 Query Match 4.1%; Score 40; DB 1; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 1,9e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 775 RWTAPPAIQRKFTSADWSYGIWMEVWSYGERPYWDM 814  
 DB 801 RWTAPPAIQRKFTSADWSYGIWMEVWSYGERPYWDM 840  
 RESULT 9  
 EPH5\_CHICK  
 ID EPH5\_CHICK STANDARD; PRT; 1002 AA.  
 AC Q07497;  
 DT 01-NOV-1997 (Rel. 35; Created)  
 DT 01-NOV-1997 (Rel. 35; Last sequence update)  
 DT 01-OCT-2000 (Rel. 40; Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
 KINASE CEK9).  
 GN EPHB5 OR CEK9.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 CC NCBI\_TaxId=9031;  
 OX NCBI\_TaxId=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97066069; PubMed=8909550;  
 RA Soans C., Holash J.A., Pavlova Y., Pasquale E.B.;  
 RT "Developmental expression and distinctive tyrosine phosphorylation of  
 the Eph-related receptor tyrosine kinase Cek9.";  
 RL J. Cell Biol. 135:781-795(1996).  
 RN [2]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RX MEDLINE=93288394; PubMed=8510926;  
 RA Sajjadi F.G., Pasquale E.B.;  
 RT "Five novel avian Eph-related tyrosine kinases are differentially  
 expressed.";  
 RL Oncogene 8:1807-1813(1993).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THYMUS AND DETECTABLE IN  
 CC BRAIN, RETINA, KIDNEY, LUNG, AND HEART. NOT DETECTED IN SKELETAL  
 CC MUSCLE AND LIVER.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

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CC EMBL: U23783; AAB41054.1; -
DR HSSP; P00523; 2PTK.
DR InterPro: IPR000561; -
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam: PF01404; EPH_Lbd; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; kinase; 1.
DR PRINTS; PR00014; FNTPEPITI.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL; 1 29
FT CHAIN; 30 1002
FT DOMAIN; 30 564 EPHRIN TYPE-B RECEPTOR 5.
FT TRANSMEM; 565 585 EXTRACELLULAR (POTENTIAL).
FT DOMAIN; 586 1002 POTENTIAL.
FT DOMAIN; 195 338 CYTOPLASMIC (POTENTIAL).
FT DOMAIN; 339 449 CYS-RICH.
FT DOMAIN; 450 547 FIBRONECTIN TYPE-III.
FT DOMAIN; 637 900 FIBRONECTIN TYPE-III.
FT DOMAIN; 862 865 PROTEIN KINASE.
FT DOMAIN; 927 1002 POLY-PRO.
FT SITE; 1000 1002 SAM.
FT BINDING; 643 651 PDZ-BINDING MOTIF (POTENTIAL).
FT BINDING; 669 669 ATP (BY SIMILARITY).
FT ACT_SITE; 762 762 ATP (BY SIMILARITY).
FT MOD_RES; 612 612 BY SIMILARITY.
FT MOD_RES; 618 618 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES; 796 796 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES; 946 946 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD; 446 446 N-LINKED (GLCNAC...) (POTENTIAL).
SO SEQUENCE 1002 AA; 111947 MW; 6D9635B500DB0DA CRC64;

Query Match 3.7%; Score 36; DB 1; Length 1002;
Best Local Similarity 100.0%; Pred. No. 4.1e-30;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 723 DMNVYHRLAARNILVNSLVCKVSDGLSRFLDD 758
Db 755 DMNVYHRLAARNILVNSLVCKVSDGLSRFLDD 790

RESULT 10
EPB3_CHICK STANDARD; PRT; 988 AA.
AC 007498;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 3 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
DE RECEPTOR CEK10) (FRAGMENT).
GN EPB3 OR CEK10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Embryo; PubMed=8510926;
RX MEDLINE=93288394;
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed."
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PRESENT IN 10-DAY EMBRYONIC BRAIN AND BODY
CC TISSUES. PROMINENT EXPRESSION IN KIDNEY, LOWER EXPRESSION IN LUNG,
CC AND BARELY DETECTABLE IN BRAIN, LIVER, HEART, SKELETAL MUSCLE AND
CC THYMUS.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z19061; CAAT9511.1; -
DR HSSP; P00523; 2PTK.
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; kinase; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF01404; EPH_Lbd; 1.
DR PRINTS; PR00014; FNTPEPITI.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Repeat.
FT NON_TER; 1 1
FT DOMAIN; <1 534 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM; 535 555 CYTOPLASMIC (POTENTIAL).
FT DOMAIN; 556 988 CYS-RICH.
FT DOMAIN; 171 308 FIBRONECTIN TYPE-III.
FT DOMAIN; 309 421 FIBRONECTIN TYPE-III.
FT DOMAIN; 422 520 FIBRONECTIN TYPE-III.
FT DOMAIN; 623 865 PROTEIN KINASE.
FT DOMAIN; 913 988 SAM.
FT SITE; 986 988 PDZ-BINDING MOTIF (POTENTIAL).
FT N_BIND; 629 637 ATP (BY SIMILARITY).
FT BINDING; 53 88 ATP (BY SIMILARITY).
FT ACT_SITE; 655 655 ATP (BY SIMILARITY).
FT MOD_RES; 748 748 BY SIMILARITY.
FT MOD_RES; 598 598 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES; 604 604 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES; 782 782 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES; 932 932 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD; 323 323 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD; 418 418 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPPLIC; 558 572 MISSING (IN SHORT ISOFORM).
SO SEQUENCE 988 AA; 109578 MW; EEA0D39C03FFD3C8 CRC64;

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Query Match 3.6%; Score 35; DB 1; Length 988;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-29;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 MNYVHRDLARNILVNSLVCKVSDGLSRLFLEDD 758  
 DB 742 MNYVHRDLARNILVNSLVCKVSDGLSRLFLEDD 776

RESULT 11

EPB3\_MOUSE STANDARD; PRT; 993 AA.

ID EPB3\_MOUSE  
 AC P54754; Q62214;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR MDK-5) (DEVELOPMENTAL KINASE 5) (SEK-4).  
 GN EPHB3 OR ETK2 OR MDK5 OR SEK4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Embryo;  
 RX MEDLINE=96074837; PubMed=7478528;  
 RA Closssek T., Lerch M.M., Ullrich A.;  
 RT "Cloning, characterization, and differential expression of MDK2 and MDK5, two novel receptor tyrosine kinases of the eck/eph family.";  
 RL Oncogene 11:2085-2095(1995).  
 [2]  
 RP SEQUENCE OF 719-993 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE=95034306; PubMed=7947319;  
 RA Becker N., Seitandou T., Murphy P., Mattei M.G., Topilko P., Nieto A., Wilkinson D.G., Charney P., Gilardi P.;  
 RT "Several receptor tyrosine kinase genes of the eph family are segmentally expressed in the developing hindbrain.";  
 RL Mech. Dev. 47:3-17(1994).  
 [3]  
 RN TISSUE SPECIFICITY.  
 RP MEDLINE=20171264; PubMed=10704386;  
 RA Tiondi R., Wideman C., Kaprielian Z.;  
 RT "Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the orientation of longitudinally projecting axons.";  
 RL Development 127:1397-1410(2000).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISK.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Z49086; CA88910.1; -;  
 DR HSSP: P00523; 2PTK.  
 DR MGD: MGI:104770; Ephb3.  
 DR InterPro: IPR000719; -;

DR InterPro: IPR001090; -;  
 DR InterPro: IPR001245; -;  
 DR InterPro: IPR001426; -;  
 DR InterPro: IPR001600; -;  
 DR InterPro: IPR001777; -;  
 DR Pfam: PF01404; EPH\_Lbd; 1.  
 DR Pfam: PF00536; SAM; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PRINTS: PR00104; FMYPELIT.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00790; RICEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RICEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR Transferrase: Tyrosine-protein kinase: ATP-binding, Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 29  
 FT CHAIN 30 993  
 FT DOMAIN 30 554  
 FT TRANSMEM 555 575  
 FT DOMAIN 576 593  
 FT DOMAIN 191 328  
 FT DOMAIN 329 443  
 FT DOMAIN 444 539  
 FT DOMAIN 628 891  
 FT DOMAIN 918 993  
 FT SITE 991 993  
 FT NP\_BIND 634 642  
 FT BINDING 660 660  
 FT ACT\_SITE 753 753  
 FT MOD\_RES 603 603  
 FT MOD\_RES 509 509  
 FT MOD\_RES 787 787  
 FT MOD\_RES 937 937  
 FT CARBOHYD 343 343  
 FT CARBOHYD 440 440  
 FT CONFLICT 719 719  
 SQ SEQUENCE 993 AA; 109585 MW; 0B66A4D391266C79 CRC64;

Query Match 3.6%; Score 35; DB 1; Length 993;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-29;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 MNYVHRDLARNILVNSLVCKVSDGLSRLFLEDD 758  
 DB 747 MNYVHRDLARNILVNSLVCKVSDGLSRLFLEDD 781

RESULT 12

EPB3\_HUMAN STANDARD; PRT; 998 AA.

ID EPB3\_HUMAN  
 AC P54753;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HEK-2).  
 GN EPHB3 OR ETK2 OR HEK2.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Embryo;  
 RX MEDLINE=93390963; PubMed=8397371;  
 RA Boehme B., Holtlich U., Wolf G., Grzeschik K.-H., Strebhardt K., Ruebsamen-Waigmann H.;  
 RT "PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.";

CC Oncogene 8:2857-2862(1993).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO  
 CC EPHRIN-B1 AND -B2.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X75208; CAAS3021.1; -  
 CC DR HSSP: P00523; 2PTK.  
 CC DR MIM: 601839; -  
 CC DR InterPro: IPR000719; -  
 CC DR InterPro: IPR001090; -  
 CC DR InterPro: IPR001245; -  
 CC DR InterPro: IPR001426; -  
 CC DR InterPro: IPR001660; -  
 CC DR InterPro: IPR001777; -  
 CC DR Pfam: PF00536; SAM\_1.  
 CC DR Pfam: PF00041; fn3; 2.  
 CC DR Pfam: PF00069; pkinase; 1.  
 CC DR PRINTS: PRO0014; ENTPEIIT.  
 CC DR PRINTS: PRO0109; TYRKINASE.  
 CC DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 CC DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 CC DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 CC DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 CC FT SIGNAL 1 33  
 CC FT CHAIN 34 998  
 CC FT DOMAIN 34 559  
 CC FT TRANSMEM 560 580  
 CC FT DOMAIN 581 998  
 CC FT DOMAIN 199 336  
 CC FT DOMAIN 337 448  
 CC FT DOMAIN 449 544  
 CC FT DOMAIN 633 896  
 CC FT DOMAIN 923 998  
 CC FT SITE 996 998  
 CC FT NE\_BIND 639 647  
 CC FT BINDING 665 665  
 CC FT ACT\_SITE 758 758  
 CC FT MOD\_RES 608 608  
 CC FT MOD\_RES 614 614  
 CC FT MOD\_RES 792 792  
 CC FT MOD\_RES 942 942  
 CC FT CARBOHYD 351 351  
 CC FT CARBOHYD 445 445  
 CC FT SEQUENCE 998 AA: 110286 MW: 576826397CC61103 CRC64;

Query Match 3.6%; Score 35; DB 1; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-29;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 724 MNYVHRDLAARNILVNSLVCKVSDFGSLRFLDD 758  
 DB 752 MNYVHRDLAARNILVNSLVCKVSDFGSLRFLDD 786

RESULT 13  
 ID EBP3\_XENLA STANDARD; PRT; 974 AA.  
 AC 091735;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
 DE KINASE RECEPTOR TCX).  
 GN TCX.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP MEDLINE=96068901; PubMed=7478602;  
 RA Scales J.B., Winning R.S., Renaud C.S., Shea L.J., Sargent T.D.;  
 RT "Novel members of the eph receptor tyrosine kinase subfamily expressed  
 RT during Xenopus development";  
 RL Oncogene 11:1745-1752(1995).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY  
 CC SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC  
 CC MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST  
 CC ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS  
 CC IN INTESTINE, KIDNEY, OVIDUCT AND PHARYNX.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: LA3620; AAA93526.1; -  
 CC DR HSSP: P29323; 1BAF.  
 CC DR InterPro: IPR000719; -  
 CC DR InterPro: IPR001090; -  
 CC DR InterPro: IPR001245; -  
 CC DR InterPro: IPR001426; -  
 CC DR InterPro: IPR001660; -  
 CC DR InterPro: IPR001777; -  
 CC DR Pfam: PF00041; fn3; 2.  
 CC DR Pfam: PF00069; pkinase; 1.  
 CC DR Pfam: PF00536; SAM\_1.  
 CC DR Pfam: PF01404; EPH\_Lbd; 1.  
 CC DR PRINTS: PRO0014; ENTPEIIT.  
 CC DR PRINTS: PRO0109; TYRKINASE.  
 CC DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 CC DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 CC DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 CC DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 CC FT SIGNAL 1 16  
 CC FT CHAIN 17 974  
 CC FT DOMAIN 17 534  
 CC FT TRANSMEM 535 555  
 CC FT DOMAIN 556 974  
 CC FT DOMAIN 178 315  
 CC FT CYTOPLASMIC (POTENTIAL).  
 CC CYS-RICH.

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FT DOMAIN 316 423 FIBRONECTIN TYPE-III.
FT DOMAIN 424 520 FIBRONECTIN TYPE-III.
FT DOMAIN 609 872 FIBRONECTIN TYPE-III.
FT DOMAIN 899 974 SAM.
FT SITE 972 974 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 615 623 ATP (BY SIMILARITY).
FT DISULFID 60 95 BY SIMILARITY.
FT BINDING 641 641 ATP (BY SIMILARITY).
FT ACT_SITE 734 734 BY SIMILARITY.
FT MOD_RES 584 584 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 590 590 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 768 768 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 918 918 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 330 330 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 974 AA; 108263 MW; F881412E86628533 CRC64;

Query Match 3.4%; Score 33; DB 1; Length 974;
Best Local Similarity 100.0%; Pred. No. 7e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 724 MNYVRDLAARNILVNSLVCVSDGLSRFLE 756
Db 728 MNYVRDLAARNILVNSLVCVSDGLSRFLE 760

RESULT 14
EPH1_CHICK STANDARD; PRT; 984 AA.
AC 007494;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
  RECEPTOR EPH-2) (TYROSINE KINASE CEK6 RECEPTOR) (FRAGMENT).
GN EPHB1 OR CEK6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
  OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE-93288394; PubMed-8510926;
RT SaJJadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
  expressed."
RT Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
  EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS
  IN THE NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
  TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE 10-DAY EMBRYO,
  AND IN ADULT BRAIN, LUNG, HEART AND SKELETAL MUSCLE. LOW LEVELS OF
  EXPRESSION DETECTED IN ALL OTHER ADULT TISSUES TESTED.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
  RECEPTOR SUBFAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z19110; CAA79526.1; -

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DR HSP: P00523; 2PTR.
DR InterPro: IPR000561; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001090; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001426; -.
DR InterPro: IPR001660; -.
DR InterPro: IPR001777; -.
DR Pfam: PF01404; EPH_1bd; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; In3; 2.
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; PARTIAL.
DR PROSITE: PS01861; RECEPTOR_TYR_KIN_V_2; 1.
DR TRANSFERASE: Tyrosine-protein kinase; Arp-binding; Phosphorylation;
  KW Receptor; Transmembrane; Glycoprotein; Repeat.
FT NON_TER 1 1
FT DOMAIN 542 541 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 542 552 POTENTIAL.
FT DOMAIN 563 984 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 164 300 CYS-RICH.
FT DOMAIN 301 410 FIBRONECTIN TYPE-III.
FT DOMAIN 411 527 FIBRONECTIN TYPE-III.
FT DOMAIN 619 882 PROTEIN KINASE.
FT DOMAIN 909 984 SAM.
FT SITE 982 984 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 625 633 ATP (BY SIMILARITY).
FT BINDING 651 651 ATP (BY SIMILARITY).
FT ACT_SITE 744 744 BY SIMILARITY.
FT MOD_RES 594 594 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 600 600 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 778 778 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 928 928 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 984 AA; 109519 MW; EF06C83BB63A13A1 CRC64;

Query Match 3.3%; Score 32; DB 1; Length 984;
Best Local Similarity 100.0%; Pred. No. 8.6e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 691 LDFSLRNDGQFTVLDVGLRGIAAGMYLA 722
Db 705 LDFSLRNDGQFTVLDVGLRGIAAGMYLA 736

RESULT 15
EPH1_HUMAN STANDARD; PRT; 984 AA.
AC P54762; O43569; O95142; O95143;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
  KINASE RECEPTOR EPH-2) (NET) (HEK6) (ELK).
GN EPHB1 OR EPHB2 OR NET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM EPHB1A).
RC TISSUE=Fetal brain;
RA MEDLINE-96115594; PubMed-8666391;
RA Tang X.X., Biegel J.A., Nycum L.M., Yoshioka A., Brodeur G.M.,
  RA Pleasure D.E., Ikegaki N.;
  RT "cDNA cloning, molecular characterization, and chromosomal
  localization of NET(EPH2), a human Eph-related receptor protein-
  RT tyrosine kinase gene preferentially expressed in brain.";
  RT Genomics 29:426-437(1995).

```

RN [12] SEQUENCE FROM N.A. (ISOFORMS EPHB1A TO EPHB1D).  
RC TISSUE-Kidney;  
RA Stein E., Schoecklmann H.O., Daniel T.O.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP INTERACTIONS WITH GRB2 AND GRB10.  
RX MEDLINE-96394464; PubMed-8798570;  
RA Stein E., Cerretti D.P., Daniel T.O.;  
RT Ligand activation of Elk receptor tyrosine kinase promotes its  
J association with Grb10 and Grb2 in vascular endothelial cells.;  
RL J. Biol. Chem. 271:23588-23593(1996).  
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO  
EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS  
IN THE NERVOUS SYSTEM.  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
PROTEIN TYROSINE PHOSPHATE.  
CC -1- SUBUNIT: THE LIGAND-ACTIVATED FORM INTERACTS WITH GRB2, GRB10 AND  
NCK THROUGH THEIR RESPECTIVE SH2 DOMAINS. THE GRB10 SH2 DOMAIN  
BINDS EPHB1 THROUGH TYR-928, WHILE GRB2 BINDS RESIDUES WITHIN THE  
CATALYTIC DOMAIN. THE NCK SH2 DOMAIN BINDS EPHB1 THROUGH TYR-594.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; EPHB1A (SHOWN HERE), EPHB1B,  
EPH1C AND EPHB1D. ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN BRAIN.  
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
RECEPTOR SUBFAMILY.  
CC -----  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; L40636; AAB08520.1; -;  
DR EMBL; AF037331; AAD02030.1; -;  
DR EMBL; AF037332; AAD02031.1; -;  
DR EMBL; AF037333; AAB94627.1; -;  
DR EMBL; AF037334; AAB94628.1; -;  
DR HSP; P00523; 2PTK.  
DR MIM; 600600; -;  
DR InterPro; IPR000561; -;  
DR InterPro; IPR000719; -;  
DR InterPro; IPR001090; -;  
DR InterPro; IPR001245; -;  
DR InterPro; IPR001426; -;  
DR InterPro; IPR001660; -;  
DR InterPro; IPR001777; -;  
DR Pfam; PF01404; EPH\_1bd; 1.  
DR Pfam; PF00536; SAM; 1.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PRO0014; ENTPEIIT.  
DR PRINTS; PRO0109; TYRKINASE.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN; 1.  
KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Alternative splicing.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 984 EPHRIN TYPE-B RECEPTOR 1.  
FT DOMAIN 18 540 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 541 563 POTENTIAL.  
FT DOMAIN 564 984 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 183 319 CYS-RICH.

FT	DOMAIN	320	429	FIBRONECTIN TYPE-III.
FT	DOMAIN	430	527	FIBRONECTIN TYPE-III.
FT	DOMAIN	619	882	PROTEIN KINASE.
FT	DOMAIN	909	984	SAM.
FT	SITE	982	984	PDZ-BINDING MOTIF (POTENTIAL).
FT	NP BIND	625	633	ATP (BY SIMILARITY).
FT	ACT_SITE	651	651	ATP (BY SIMILARITY).
FT	ACT_SITE	744	744	BY SIMILARITY.
FT	MOD_RES	594	594	PHOSPHORYLATION (AUTO-).
FT	MOD_RES	600	600	PHOSPHORYLATION (AUTO-).
FT	MOD_RES	708	778	PHOSPHORYLATION (AUTO-).
FT	MOD_RES	928	928	PHOSPHORYLATION (AUTO-).
FT	CARBOHYD	334	334	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	426	426	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	480	480	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	480	480	MALDYLILLLASVAMEETLMDTRT -> METREKKRSR
FT	VARSPLIC	1	27	AEEGTR (IN ISOFORM EPHB1B).
FT	VARSPLIC	617	984	MISSING (IN ISOFORM EPHB1D).
FT	VARSPLIC	642	682	MISSING (IN ISOFORM EPHB1C).
FT	CONFLICT	12	12	A -> E (IN REF. 2).
FT	CONFLICT	87	87	T -> S (IN REF. 2).
FT	CONFLICT	152	152	G -> R (IN REF. 2).
FT	CONFLICT	185	185	S -> I (IN REF. 2).
FT	CONFLICT	274	274	T -> R (IN REF. 2).
FT	CONFLICT	336	336	T -> S (IN REF. 2).
FT	CONFLICT	367	367	R -> G (IN REF. 2).
FT	CONFLICT	485	485	R -> S (IN REF. 2).
FT	CONFLICT	813	813	V -> H (IN REF. 2).
FT	CONFLICT	819	819	S -> Y (IN REF. 2).
FT	CONFLICT	847	847	M -> T (IN REF. 2).
FT	CONFLICT	973	973	R -> W (IN REF. 2).
SO	SEQUENCE	984 AA;	109884 MW;	8044160E24E93A92 CRC64;

Query Match 3.3%; Score 32; DB 1; Length 984;  
Best Local Similarity 100.0%; Pred. No. 8.6e-26;  
Matches 32; Conservative 0; Mismatches 0; Indels 0;  
QY 691 LDSELRNDGQFTVYIQLVGMRLGIAAGMKYLA 722  
Db 705 LDSELRNDGQFTVYIQLVGMRLGIAAGMKYLA 736

Search completed: July 24, 2001, 16:36:54  
Job time: 205 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:33:04 ; Search time 34.37 Seconds

(without alignments)  
3733.950 Million cell updates/sec

Title: US-09-378-759-11

Sequence: 1 LIAAVEEILMDSTATAEIG.....IINSTQVMPAQMNIQSVSEV 970

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_UNCLASSIFIED:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_VIRUS:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322	33.2	994	11	Q9GVY4 mus sp. neu
2	296	30.5	552	4	Q9H4H4 Q9H4H4 homo sapien
3	295	30.4	621	4	Q9H4H3 Q9H4H3 homo sapien
4	54	5.6	815	13	Q9H4H3 Q9H4H3 homo sapien
5	47	4.8	353	13	Q9PVV2 lampetra re
6	40	4.1	353	13	Q9PVV2 lampetra re
7	39	4.0	353	13	Q9U8W2 Q9U8W2 mus musculu
8	35	3.6	938	11	Q60669 Q60669 mus musculu
9	31	3.2	880	13	Q73878 Q73878 brachydanio
10	30	3.1	987	13	Q73875 Q73875 brachydanio
11	29	3.0	323	13	Q91734 Q91734 xenopus lae
12	29	3.0	976	13	Q73878 Q73878 brachydanio
13	29	3.0	977	13	Q9PWR5 Q9PWR5 xenopus lae
14	28	2.9	334	4	Q9U564 Q9U564 homo sapien
15	21	2.2	57	13	Q91564 Q91564 xenopus lae
16	20	2.1	490	13	Q73877 Q73877 brachydanio
17	19	2.0	353	13	Q9U8W9 Q9U8W9 eptatretus
18	19	2.0	853	4	Q9P269 Q9P269 homo sapien
19	19	2.0	1005	4	Q9NUA9 Q9NUA9 homo sapien

20	18	1.9	348	13	Q9U8W0 Q9U8W0 eptatretus
21	17	1.8	349	13	Q9U8W1 Q9U8W1 eptatretus
22	17	1.8	350	13	Q9PVV1 Q9PVV1 lampetra re
23	16	1.6	983	4	Q9H2V4 Q9H2V4 homo sapien
24	15	1.5	57	11	Q61821 Q61821 mus musculu
25	15	1.5	977	11	Q9ESJ2 Q9ESJ2 mus musculu
26	14	1.4	74	11	Q62128 Q62128 mus musculu
27	14	1.4	390	5	Q9U8V8 Q9U8V8 branchiost
28	14	1.4	1035	5	Q9XZL6 Q9XZL6 drosophila
29	14	1.4	1047	5	Q917D4 Q917D4 drosophila
30	14	1.4	1080	5	Q9Y1J0 Q9Y1J0 drosophila
31	14	1.4	1096	5	Q9V4E5 Q9V4E5 drosophila
32	13	1.3	342	5	Q9U8V7 Q9U8V7 branchiost
33	13	1.3	666	13	Q73876 Q73876 brachydanio
34	13	1.3	893	5	Q9Y1Y3 Q9Y1Y3 ephydalia f
35	13	1.3	1019	5	Q96435 Q96435 drosophila
36	13	1.3	1126	13	Q9PWN6 Q9PWN6 cyprinus ca
37	12	1.2	57	13	Q91999 Q91999 xenopus lae
38	12	1.2	62	5	Q61292 Q61292 anthocidari
39	12	1.2	67	5	Q25192 Q25192 hydra atten
40	12	1.2	237	5	Q25196 Q25196 hydra atten
41	12	1.2	435	4	Q15850 Q15850 homo sapien
42	12	1.2	465	4	Q16176 Q16176 homo sapien
43	12	1.2	465	11	P70223 P70223 mus musculu
44	12	1.2	503	4	Q15250 Q15250 homo sapien
45	12	1.2	511	11	Q64103 Q64103 mus musculu

## ALIGNMENTS

RESULT 1  
ID Q9GVY4 PRELIMINARY: PRT: 994 AA.  
AC Q9GVY4:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE NEURAL KINASE, NUK=EPH/ELK FAMILY RECEPTOR-LIKE TYROSINE KINASE.  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94181250; PubMed=8134103;  
RA Henkemeyer M., Marangere L.E., McGlade J., Olivier J.P., Conlon R.A.,  
RT Holmyard D.P., Letwin K., Pawson T.,  
RT Immunolocalization of the Nuk receptor tyrosine kinase suggests roles  
RT in segmental patterning of the brain and axonogenesis.";  
RL Oncogene 9:1001-1014(1994).  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
CC TYROSINE PHOSPHATE (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
CC RECEPTOR SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC HSSP: P06239; 3LCK.  
CC InterPro: IPR000561; -  
CC InterPro: IPR000719; -  
CC InterPro: IPR001090; -  
CC InterPro: IPR001245; -  
CC InterPro: IPR001426; -  
CC InterPro: IPR001660; -  
CC InterPro: IPR001777; -  
CC Pfam: PF00041; fn3; 2.  
CC Pfam: PF00069; pkinase; 1.  
CC Pfam: PF00536; SAM; 1.  
CC Pfam: PF01404; Eph\_1bd; 1.  
CC PRINTS: PR00014; ENTYPETIT.  
CC PRINTS: PR00109; TYRKINASE.  
CC PROSITE: PS01186; EGF\_2; UNKNOWN 1.  
CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: P550011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: P500109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: P500790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE: P500791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR SMART: SM00454; SAM; 1.  
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;  
KW Transferase; Transmembrane; Tyrosine-protein kinase.  
SQ SEQUENCE 994 AA; 110759 MW; BC6B9B12A070394C CRC64.

Query Match 33.2%; Score 322; DB 11; Length 994;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 GFLAIFODYGGKNSLAVRVYRKCPRIIONGAIFOETISGASTSLVAARGSCIANAE 218  
DB 181 GFLAIFODYGGKNSLAVRVYRKCPRIIONGAIFOETISGASTSLVAARGSCIANAE 240  
QY 219 VDPPIKLYCGDDEMLVPIGRCKMKAGFEAVENGTCRCGPGSTFRANOGDEACTHCPI 278  
DB 241 VDPPIKLYCGDDEMLVPIGRCKMKAGFEAVENGTCRCGPGSTFRANOGDEACTHCPI 300  
QY 279 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 338  
DB 301 SRTTSGATNCVCRNGYRRADLPDLPCTTISAPQAVISSVNETSLMEWTPPRDSG 360  
QY 339 REDLVNIITCKSCGSGRACRCGDNVQYAPROLGLTEPRITYSDLLAHTQYTFEIOAVN 398  
DB 361 REDLVNIITCKSCGSGRACRCGDNVQYAPROLGLTEPRITYSDLLAHTQYTFEIOAVN 420  
QY 399 GVTDOSPEFQFASVNTTMOAPSAVSIMHOYSRTVDSITLMSOPDOPNGVILLYELO 458  
DB 421 GVTDOSPEFQFASVNTTMOAPSAVSIMHOYSRTVDSITLMSOPDOPNGVILLYELO 480  
QY 459 YRKELSEYNATAIKSPNTVT 480  
DB 481 YRKELSEYNATAIKSPNTVT 502

RESULT 2  
Q9HAH4 PRELIMINARY; PRT; 552 AA.  
AC Q9HAH4;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE DJ74M1.1.1 (TYROSINE KINASE ISOFORM 1) (FRAGMENT).  
GN EPHB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bagguley C.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL035704; CAC10350.1; -  
KW Kinase.  
FT NON\_TER 1 1  
SQ SEQUENCE 552 AA; 62206 MW; D643D1C857B1A3DB CRC64;

Query Match 30.5%; Score 296; DB 4; Length 552;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 633  
DB 156 TPGMKIYIDPFYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 215  
QY 634 VAITLKSYTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 693  
DB 216 VAITLKSYTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 275

QY 694 FLRONDGQFTYIQLVGMRLGIAAGKXYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 753  
DB 276 FLRONDGQFTYIQLVGMRLGIAAGKXYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 335  
QY 754 FLEDDTSPTYSALGKPIRMTAPEALIQYRKFTSASDVMSYGIWMVMSYGERPYWD 813  
DB 336 FLEDDTSPTYSALGKPIRMTAPEALIQYRKFTSASDVMSYGIWMVMSYGERPYWD 395  
QY 814 MTNODVINAIEODYELPPMDCPSALHQLMDCWOKDRNRHPRFGQIYNTLDKMRNPS 873  
DB 396 MTNODVINAIEODYELPPMDCPSALHQLMDCWOKDRNRHPRFGQIYNTLDKMRNPS 455  
QY 874 LKAMAPLSSGINLPILDRITPDYTSFNVDWMLAIKMGQYKESFANAGFTSFVVSQMM 933  
DB 456 LKAMAPLSSGINLPILDRITPDYTSFNVDWMLAIKMGQYKESFANAGFTSFVVSQMM 515  
QY 934 MEDILRVGVTLAGHCKKILNSIQVMRAQNOIQSVEV 970  
DB 516 MEDILRVGVTLAGHCKKILNSIQVMRAQNOIQSVEV 552

RESULT 3  
Q9HAH3 PRELIMINARY; PRT; 621 AA.  
AC Q9HAH3;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE DJ74M1.1.2 (TYROSINE KINASE ISOFORM 2) (FRAGMENT).  
GN EPHB2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bagguley C.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL035704; CAC10351.1; -  
KW Kinase.  
FT NON\_TER 1 1  
SQ SEQUENCE 621 AA; 69824 MW; 3DA410CEB04979BF CRC64;

Query Match 30.4%; Score 295; DB 4; Length 621;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 TPGMKIYIDPFYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 633  
DB 156 TPGMKIYIDPFYEDPNEAVREFAKEIDISCVKIEQVIGAGEGEVCSGHLKLPGRKEIF 215  
QY 634 VAITLKSYTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 693  
DB 216 VAITLKSYTEKORDFLSEASIMGOFDHPNVIHLEGVYTKSPVVIITEFMENGLDS 275  
QY 694 FLRONDGQFTYIQLVGMRLGIAAGKXYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 753  
DB 276 FLRONDGQFTYIQLVGMRLGIAAGKXYLADNMYVHRDLAARILVNSNLYCKVSPFGLSR 335  
QY 754 FLEDDTSPTYSALGKPIRMTAPEALIQYRKFTSASDVMSYGIWMVMSYGERPYWD 813  
DB 336 FLEDDTSPTYSALGKPIRMTAPEALIQYRKFTSASDVMSYGIWMVMSYGERPYWD 395  
QY 814 MTNODVINAIEODYELPPMDCPSALHQLMDCWOKDRNRHPRFGQIYNTLDKMRNPS 873  
DB 396 MTNODVINAIEODYELPPMDCPSALHQLMDCWOKDRNRHPRFGQIYNTLDKMRNPS 455  
QY 874 LKAMAPLSSGINLPILDRITPDYTSFNVDWMLAIKMGQYKESFANAGFTSFVVSQMM 933  
DB 456 LKAMAPLSSGINLPILDRITPDYTSFNVDWMLAIKMGQYKESFANAGFTSFVVSQMM 515

QY 934 MEDLRVGVTLGAGHOKILNSIOVMRAQMOIOSVE 969  
DB 516 MEDLRVGVTLGAGHOKILNSIOVMRAQMOIOSVE 551

## RESULT 4

OS 057458 PRELIMINARY; PRT; 815 AA.  
AC 057458;  
DT 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE EPHB2-TYROSINE KINASE RECEPTOR (FRAGMENT).  
GN XEPHB2.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355.

RA Tanaka M., Wang D.Y., Kamo T., Igarashi H., Wang Y., Xiang Y.Y.,  
RA Tanaka F., Naitoh Y., Sugimura H.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
CC TYROSINE PHOSPHATE (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
CC RECEPTOR SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC EMBL: AB026039; AAB94603.1; -.  
DR HSP: P29323; 184F.  
DR InterPro: IPR000561; -.  
DR InterPro: IPR000719; -.  
DR InterPro: IPR001245; -.  
DR InterPro: IPR001426; -.  
DR InterPro: IPR001660; -.  
DR InterPro: IPR001777; -.  
DR Pfam: PF00041; fn3; 2.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00536; SAM; 1.  
DR PRINTS: PRO0014; FNTYPEIT.  
DR PRINTS: PRO0109; TYRKINASE.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR SMART: SM00454; SAM; 1.  
KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;  
KW Transferase; Transmembrane; Tyrosine-protein kinase.  
FT NON\_TER  
SQ SEQUENCE 815 AA; 90848 MW; D36D77C498097BFE CRC64;

Query Match 5.6%; Score 54; DB 13; Length 815;  
Best Local Similarity 100.0%; Pred. No. 5.6e-48;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TPGMKIYIDFTEDPNEAVREFAKEDISCVKIEOVIGAGEGECVSGHLKLP 627  
DB 419 TPGMKIYIDFTEDPNEAVREFAKEDISCVKIEOVIGAGEGECVSGHLKLP 472

## RESULT 5

OS 09PVV2 PRELIMINARY; PRT; 353 AA.  
AC 09PVV2;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE EPHB (FRAGMENT).

OS Lampetra reissneri.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lampetra.  
OX NCBI\_TaxID=7553;

RA Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;  
RT "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey;  
RT Isoform duplications around the divergence of cyclostomes and  
RT gnathostomes".  
RL J. Mol. Evol. 49:601-608(1999).  
DR EMBL: AB025542; BAA84732.1; -.  
DR HSP: P06239; 3LCK.  
DR InterPro: IPR000719; -.  
DR InterPro: IPR001245; -.  
DR InterPro: IPR001660; -.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00536; SAM; 1.  
DR PRINTS: PRO0109; TYRKINASE.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR SMART: SM00454; SAM; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
FT NON\_TER  
SQ SEQUENCE 353 AA; 39797 MW; 034B315DA02BED8D CRC64;

Query Match 4.8%; Score 47; DB 13; Length 353;  
Best Local Similarity 100.0%; Pred. No. 7.2e-41;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 PVMIITEFMENGSLDSFLRNDGQFTYIQLVGMIRGIAAGMKYLA DM 724  
DB 61 PVMIITEFMENGSLDSFLRNDGQFTYIQLVGMIRGIAAGMKYLA DM 107

OS 09PSK9 PRELIMINARY; PRT; 60 AA.  
AC 09PSK9;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE PROTEIN KINASE.  
OS Gallus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93096482; PubMed=1281306;  
RA Marcelle C., Eichmann A.;  
RT "Molecular cloning of a family of protein kinase genes expressed in  
RT the avian embryo".  
RL Oncogene 7:2479-2487(1992).  
DR HSP: P12931; 1FMK.  
DR InterPro: IPR000719; -.  
DR Pfam: PF00069; pkinase; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Transferase.  
SQ SEQUENCE 60 AA; 6593 MW; EA947B9C0857B243 CRC64;

Query Match 4.1%; Score 40; DB 13; Length 60;  
Best Local Similarity 100.0%; Pred. No. 3.9e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 AARNIIIVNSLVCKVSDFGISRLFEDTSDPTYSALGK 771  
DB 1 AARNIIIVNSLVCKVSDFGISRLFEDTSDPTYSALGK 40

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RESULT 7
ID Q908W2 PRELIMINARY; PRT; 353 AA.
AC Q908W2;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE EPHB (FRAGMENT).
OC Eptarectus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotretli; Myxiniiformes;
OC Myxiniidae; Eptarectinae; Eptarectus.
OX NCBI_TaxId=7764;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20020330; PubMed=10552041;
RA Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;
RT "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey;
RT isoform duplications around the divergence of cyclostomes and
RT gnathostomes.";
RL J. Mol. Evol. 49:601-608(1999).
DR EMBL; AB025538; BAA84728.1; -.
DR HSSP; P00523; 2PTK.
DR InterPro; IPR000719; -.
DR InterPro; IPR001245; -.
DR InterPro; IPR001660; -.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR SMART; SM00454; SAM; 1.
DR ATP-binding; Transferase; Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 353 AA; 39821 MW; 239E5B953698402A CRC64;

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Query Match 4.0%; Score 39; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.3e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 686 MENGSLDSELRNDGQFTVYIOLVGMRLGIAAGKRYLADM 724
    |||||||||||||||||||||||||||||||||||||||
DB 69 MENGSLDSELRNDGQFTVYIOLVGMRLGIAAGKRYLADM 107

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RESULT 8
ID Q60669 PRELIMINARY; PRT; 938 AA.
AC Q60669;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE PROTEIN KINASE (FRAGMENT).
OS EPHB3 OR ETK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95200798; PubMed=7893599;
RA Ruiz J.C., Conlon F.L., Robertson E.J.;
RT "Identification of novel protein kinases expressed in the myocardium
RT of the developing mouse heart.";
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE (BY SIMILARITY).
CC -1- SUPRACELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL; U11493; AAA67925.1; -.

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DR HSSP; P29323; 1BAF.
DR MGD; MGI:104770; Ephb3.
DR InterPro; IPR000719; -.
DR InterPro; IPR001090; -.
DR InterPro; IPR001245; -.
DR InterPro; IPR001426; -.
DR InterPro; IPR001660; -.
DR InterPro; IPR001777; -.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF01404; EPH_lbd; 1.
DR PRINTS; PR00014; ENYPERILI.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR SMART; SM00454; SAM; 1.
DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 938 AA; 103996 MW; 8D128CA46f19E73F CRC64;

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Query Match 3.6%; Score 35; DB 11; Length 938;
Best Local Similarity 100.0%; Pred. No. 9.9e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 724 MNVHRDLAARNILVNSNLVCVSDFGLSRFLDD 758
    |||||||||||||||||||||||||||||||||||||||
DB 692 MNVHRDLAARNILVNSNLVCVSDFGLSRFLDD 726

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RESULT 9
ID Q73879 PRELIMINARY; PRT; 880 AA.
AC Q73879;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
GN RTK4.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Cooke J.E., Xu Q., Wilson S.W., Holder N.;
RA dev. Genes Evol. 206:515-531(1997).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE (BY SIMILARITY).
CC -1- SUPRACELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL; AJ005030; CAA06303.1; -.
DR HSSP; P00523; 2PTK.
DR ZFIN; ZDB-GENE-990415-61; rtk4.
DR InterPro; IPR000561; -.
DR InterPro; IPR000719; -.
DR InterPro; IPR001090; -.
DR InterPro; IPR001245; -.
DR InterPro; IPR001426; -.
DR InterPro; IPR001660; -.
DR InterPro; IPR001777; -.

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DR Pfam: PF00064: fn3.2.  
 DR Pfam: PF00069: Pkinase.1.  
 DR Pfam: PF01404: Eph\_1bd.1.  
 DR PRINTS: PR00014: FNTYPEIIT.  
 DR PRINTS: PR00109: TYRKINASE.  
 DR PROSITE: PS01186: EGF\_2: UNKNOWN.1.  
 DR PROSITE: PS01017: PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS50011: PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00109: PROTEIN\_KINASE\_TYR.1.  
 DR PROSITE: PS00790: RECEPTOR\_TYR\_KIN\_V.1.  
 DR PROSITE: PS00791: RECEPTOR\_TYR\_KIN\_V.2.1.  
 DR SMART: SM00219: TYRKC.1.  
 KM ATP-binding: Glycocyproline: Phosphorylation; Receptor; Repeat;  
 FT Transferase: Transmembrane; Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 880 AA: 98862 MW: 8875013FBI79B70B CRC64;

Query Match 3.2%; Score 31; DB 13; Length 880;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-23;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 784 YRKFTSASDVMSYGIWMEVMSYGERPYWDM 814  
 DB 741 YRKFTSASDVMSYGIWMEVMSYGERPYWDM 771

RESULT 10  
 ID 073875 PRELIMINARY; PRT; 987 AA.  
 AC 073875;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK5.  
 OS Brachydanio rerio (Zebrafish) (Zebrafish danielo).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA COOKE J.E., Xu Q., Wilson S.W., Holder N.;  
 RT "Characterisation of five novel zebrafish eph-related receptor  
 RT tyrosine kinases suggests roles in patterning the neural plate.";  
 RL Dev. Genes Evol. 206:515-531(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Pubmed-1171340;  
 RA Cooke J.E., Moens C.B., Roth L.W.A., Durbin L., Shlomi K., Brennan C.,  
 RT "Eph signalling functions downstream of Val to regulate cell sorting  
 RT and boundary formation in the caudal hindbrain.";  
 RL Development 128:571-580(2001).  
 DR EMBL: AJ005026; CAA06299.2;  
 DR InterPro: IPR000719;  
 DR InterPro: IPR001090;  
 DR InterPro: IPR001245;  
 DR InterPro: IPR001660;  
 DR InterPro: IPR001777;  
 DR Pfam: PF00064: fn3.2.  
 DR Pfam: PF00069: Pkinase.1.  
 DR Pfam: PF00536: SAM.1.  
 DR Pfam: PF01404: Eph\_1bd.1.  
 DR PRINTS: PR00109: TYRKINASE.  
 DR PRODOM: PD001495; 1.  
 DR PROSITE: PS00107: PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS50011: PROTEIN\_KINASE\_DOM.1.  
 DR SMART: SM00454: SAM.1.  
 KM Receptor; kinase.  
 SQ SEQUENCE 987 AA: 109547 MW: 1099FC1410A84918 CRC64;

Query Match 3.1%; Score 30; DB 13; Length 987;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-22;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 726 YVHRDLARNLVNSNLCKVSDGLSRFL 755  
 DB 742 YVHRDLARNLVNSNLCKVSDGLSRFL 771

RESULT 11  
 ID 091734 PRELIMINARY; PRT; 323 AA.  
 AC 091734;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE EPH RECEPTOR TYROSINE KINASE (EC 2.7.1.112) (PL7A) (FRAGMENT).  
 GN G51.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96068901; Pubmed-7478602;  
 RA Scales J.B., Manning R.S., Renaud C.S., Shea L.J., Sargent T.D.;  
 RT "Novel members of the eph receptor tyrosine kinase subfamily expressed  
 RT during xenopus development.";  
 RL Oncogene 11:1745-1752(1995).  
 RN [2]  
 RP SEQUENCE OF 84-142 FROM N.A.  
 RC TISSUE-EMBRYO;  
 RX MEDLINE-95383727; Pubmed-7655077;  
 RA Brandt A.W., Kirschner M.W.;  
 RT "Molecular cloning of tyrosine kinases in the early Xenopus embryo:  
 RT identification of eph-related genes expressed in cranial neural crest  
 RT cells of the second (hyoid) arch.";  
 RL Dev. Dyn. 203:119-140(1995).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED THROUGH THE HEAD AND IN THE TIP OF  
 CC THE EMBRYO TAIL. EXTREMELY LOW AND UBIQUITOUS EXPRESSION IN ADULT  
 CC TISSUES.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.  
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.  
 DR EMBL: L43622; AAA93525.1;  
 DR EMBL: U11728; AAA91291.1;  
 DR HSPB: P29323; 184F.  
 DR InterPro: IPR000719;  
 DR InterPro: IPR001245;  
 DR InterPro: IPR001660;  
 DR Pfam: PF00069: Pkinase.1.  
 DR Pfam: PF00536: SAM.1.  
 DR PRINTS: PR00109: TYRKINASE.  
 DR PROSITE: PS50011: PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00109: PROTEIN\_KINASE\_TYR.1.  
 DR SMART: SM00454: SAM.1.  
 KM Transferase; Tyrosine-protein kinase; Phosphorylation.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 219 PROTEIN KINASE.  
 FT ACT\_SITE 81 81 BY SIMILARITY.  
 FT MOD\_RES 115 115 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 SQ SEQUENCE 323 AA: 36518 MW: C59800A76BA388B2 CRC64;

Query Match 3.0%; Score 29; DB 13; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-22;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 727 VHRDLAARNILVNSLVCKVSDFGLSRFL 755  
 DB 78 VHRDLAARNILVNSLVCKVSDFGLSRFL 106

RESULT 12  
 ID 073878 PRELIMINARY; PRT; 976 AA.  
 AC 073878;  
 DT 01-AUG-1998 (TREMBLERL. 07, Created)  
 DT 01-AUG-1998 (TREMBLERL. 07, Last sequence update)  
 DT 01-MAR-2001 (TREMBLERL. 16, Last annotation update)  
 DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK8.  
 GN RTK8.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cooke J.E., Xu Q., Wilson S.W., Holder N.;  
 RL Dev. Genes Evol. 206:515-531(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Durbin L., Brennan C., Shiomi K., Cooke J., Barrios A.,  
 RA Shanmugalingam S., Guthrie B., Wilson S., Lindberg R., Holder N.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ005029; CA06302.1; -.  
 DR HSSP; P00523; 2PTK.  
 DR ZFIN; ZDB-GENE-990415-65; rtk8.  
 DR InterPro: IPR000561; -.  
 DR InterPro: IPR000719; -.  
 DR InterPro: IPR001090; -.  
 DR InterPro: IPR001245; -.  
 DR InterPro: IPR001660; -.  
 DR InterPro: IPR001777; -.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; PKinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR Pfam; PF01404; EPH\_Lbd; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; -. 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR SMART; SM00454; SAM; 1.  
 DR ATP-binding; EGF-like domain; Glycoprotein; Transferase;  
 KM tyrosine-protein kinase.  
 SQ SEQUENCE 976 AA; 108180 MW; 4619754A38B0B1F CRC64;

Query Match 3.0%; Score 29; DB 13; Length 976;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-21;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 727 VHRDLAARNILVNSLVCKVSDFGLSRFL 755  
 DB 735 VHRDLAARNILVNSLVCKVSDFGLSRFL 763  
 RESULT 13  
 ID 09PWR5 PRELIMINARY; PRT; 977 AA.  
 AC 09PWR5;  
 DT 01-MAY-2000 (TREMBLERL. 13, Created)  
 DT 01-MAY-2000 (TREMBLERL. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBLERL. 16, Last annotation update)  
 DE EPH RECEPTOR TYROSINE KINASE PRECURSOR.  
 GN EPHA2.  
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA MEDLINE=99077686; PubMed=9858686;  
 RA Heibling P.M., Tran C.T., Brandt A.W.;  
 RT Requirement for Epha receptor signaling in the segregation of Xenopus  
 RT third and fourth arch neural crest cells.  
 RL Mech. Dev. 78:63-79(1998).  
 CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE (BY SIMILARITY).  
 CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN KINASES. EPHRIN  
 CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.  
 CC RECEPTOR SUBFAMILY.  
 CC -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 DR EMBL; AJ002493; CA05500.1; -.  
 DR HSSP; P08631; IAD5.  
 DR InterPro: IPR000561; -.  
 DR InterPro: IPR000719; -.  
 DR InterPro: IPR001090; -.  
 DR InterPro: IPR001245; -.  
 DR InterPro: IPR001426; -.  
 DR InterPro: IPR001660; -.  
 DR InterPro: IPR001777; -.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; PKinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR Pfam; PF01404; EPH\_Lbd; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; -. 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR SMART; SM00454; SAM; 1.  
 DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Signal;  
 KM tyrosine-protein kinase.  
 KW transferase; Transmembrane; Tyrosine-protein kinase.  
 FT SIGNAL 1 24 EPH RECEPTOR TYROSINE KINASE.  
 FT CHAIN 25 977 POTENTIAL.  
 SQ SEQUENCE 977 AA; 109593 MW; 9931C19031A55F1D CRC64;

Query Match 3.0%; Score 29; DB 13; Length 977;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-21;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 784 YRKFTSASDVWYSGIYVMEVWYSGERYW 812  
 DB 792 YRKFTSASDVWYSGIYVMEVWYSGERYW 820

RESULT 14  
 ID 09UF33 PRELIMINARY; PRT; 334 AA.  
 AC 09UF33;  
 DT 01-MAY-2000 (TREMBLERL. 13, Created)  
 DT 01-MAY-2000 (TREMBLERL. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBLERL. 16, Last annotation update)  
 DE HYPOTHETICAL 37.3 KDA PROTEIN.  
 GN DKF2P434C1418.  
 OS Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL133666; CAB63775.1; -.  
 DR InterPro; IPR000719; -.  
 DR InterPro; IPR001245; -.  
 DR Pfam; PF00069; pkinase.1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR.1.  
 DR SMART; SM00219; Tyrc; 1.  
 KW ATP-binding; Hypothetical protein; Transferase;  
 KW Tyrosine-protein kinase.  
 SO SEQUENCE 334 AA; 37274 MW; DF89BC8423AC1A60 CRC64;

Query Match 2.9%; Score 28; DB 4; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 726 YVHRDLAARNILVNSLVCKVSDGFLSR 753  
 Db 280 YVHRDLAARNILVNSLVCKVSDGFLSR 307

RESULT 15  
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 AC Q91564;  
 DT 01-NOV-1996 (TRENBLER. 01, Created)  
 DT 01-NOV-1996 (TRENBLER. 01, Last sequence update)  
 DT 01-MAR-2001 (TRENBLER. 16, Last annotation update)  
 DE PROTEIN-TYROSINE KINASE (E17) (FRAGMENT).  
 GN E17.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=6355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95383727; PubMed=7655077;  
 RA Brandl A.W., Kirschner M.W.;  
 RT "Molecular cloning of tyrosine kinases in the early Xenopus embryo:  
 RT identification of Eck-related genes expressed in cranial neural crest  
 RT cells of the second (hyoid) arch."  
 RL Dev. Dyn. 203:119-140(1995).  
 DR EMBL; 011721; AAA91284.1; -.  
 DR InterPro; IPR000719; -.  
 DR Pfam; PF00069; pkinase.1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM.1.  
 KW ATP-binding; Transferase; Tyrosine-protein kinase.  
 FT NON\_TER 1  
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 SO SEQUENCE 57 AA; 6231 MW; 7363203E6101D00 CRC64;

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 Db 1 ARNITVNSLVCKVSDGFLSR 21

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 Job time: 207 sec

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## OM protein - protein search, using sw model

Run on: July 24, 2001, 16:23:24 ; Search time 16.3 Seconds

(without alignments)  
1198.791 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 5116  
Sequence: 1 LIAAEEFLMSTRTATLGLG.....ILNSTQVMRAQMNQISVEY 970

## Scoring table:

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Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:\*

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- 2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCNUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	5116	100.0	970	2	US-08-449-645A-11	Sequence 11, Appl
2	5116	100.0	970	2	US-08-702-367A-11	Sequence 11, Appl
3	5116	100.0	970	5	PCR-US95-04681-11	Sequence 11, Appl
4	5082	99.3	994	4	US-08-547-635-2	Sequence 2, Appl
5	4950.5	96.8	995	1	US-08-162-809-12	Sequence 18, Appl
6	4934.5	96.5	1011	1	US-08-162-809-12	Sequence 12, Appl
7	4919.5	96.2	995	2	US-08-673-789-5	Sequence 5, Appl
8	3909.5	76.4	984	2	US-08-673-789-5	Sequence 6, Appl
9	3706.5	72.4	951	1	US-08-162-809-2	Sequence 2, Appl
10	3656	71.5	973	1	US-08-162-809-10	Sequence 10, Appl
11	3649.5	71.3	988	1	US-08-162-809-14	Sequence 14, Appl
12	3632.5	71.0	998	2	US-08-449-645A-20	Sequence 20, Appl
13	3632.5	71.0	998	2	US-08-702-367A-20	Sequence 20, Appl
14	3632.5	71.0	998	5	PCR-US95-04681-20	Sequence 20, Appl
15	3595.5	70.3	970	2	US-08-673-789-7	Sequence 7, Appl
16	3590.5	70.2	993	1	US-08-348-143-1	Sequence 1, Appl
17	3590.5	70.2	993	1	US-08-571-785-1	Sequence 1, Appl
18	3326.5	63.0	973	1	US-08-162-809-8	Sequence 8, Appl
19	3035	59.3	986	2	US-08-673-789-3	Sequence 3, Appl
20	3031	59.2	967	2	US-08-449-645A-30	Sequence 30, Appl
21	3031	59.2	967	2	US-08-702-367A-30	Sequence 30, Appl
22	3031	59.2	986	2	US-08-449-645A-15	Sequence 15, Appl
23	3031	59.2	986	2	US-08-702-367A-15	Sequence 15, Appl
24	3031	59.2	986	5	PCR-US95-04681-15	Sequence 15, Appl
25	3031	59.2	991	2	US-08-449-645A-13	Sequence 13, Appl
26	3031	59.2	991	2	US-08-702-367A-13	Sequence 13, Appl
27	3031	59.2	991	5	PCR-US95-04681-13	Sequence 13, Appl

28	3024	59.1	1104	1	US-08-222-616-36	Sequence 36, Appl
29	3024	59.1	1104	5	PCR-US95-04228-36	Sequence 36, Appl
30	3016	59.0	998	2	US-08-449-645A-17	Sequence 17, Appl
31	3016	59.0	998	2	US-08-702-367A-17	Sequence 17, Appl
32	3016	59.0	998	5	PCR-US95-04681-17	Sequence 17, Appl
33	3001	58.7	998	5	PCR-US96-00419-2	Sequence 2, Appl
34	2912.5	56.9	983	2	US-08-449-645A-21	Sequence 21, Appl
35	2912.5	56.9	983	2	US-08-702-367A-21	Sequence 21, Appl
36	2912.5	56.9	983	5	PCR-US95-04681-21	Sequence 16, Appl
37	2910	56.9	983	1	US-08-162-809-16	Sequence 16, Appl
38	2909.5	56.9	983	1	US-08-167-919A-10	Sequence 10, Appl
39	2909.5	56.9	983	3	US-08-715-106-10	Sequence 10, Appl
40	2907	56.8	1005	2	US-08-469-537A-103	Sequence 103, App
41	2902.5	56.7	982	2	US-08-673-789-4	Sequence 4, Appl
42	2827.5	55.3	987	1	US-08-436-044-6	Sequence 6, Appl
43	2827.5	55.3	987	2	US-08-436-054-6	Sequence 6, Appl
44	2827.5	55.3	987	5	PCR-US95-08812-6	Sequence 6, Appl
45	2827.5	55.3	1276	1	US-08-222-616-24	Sequence 24, Appl

## ALIGNMENTS

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RESULT
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US-08-449-645A-11
; Sequence 11, Application US/08449645A
; Patent No. 5981245
; GENERAL INFORMATION:
; APPLICANT: FOX, Gary M.
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Amgen Patent Operations/RBW
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645A-11

Query Match 100.0%; Score 5116; DB 2; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIAAEEFLMSTRTATLGLGMMVHPSPGMEVSGYDENMNTIRTYOCNVPESSQNMMLR 60
DB 1 LIAAEEFLMSTRTATLGLGMMVHPSPGMEVSGYDENMNTIRTYOCNVPESSQNMMLR 60
OY 61 TKFIRRAHRIHVMKFSVDCSSIPSPGSKETFLNLYYEA DFDSATRTFPNMENP 120
DB 61 TKFIRRAHRIHVMKFSVDCSSIPSPGSKETFLNLYYEA DFDSATRTFPNMENP 120
OY 121 WKVDITADESFQVDLGGKVMKINTEVRSFGFVLAFODYGGCSILIAVAVFY 180
```

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Db 121 WKVDTIADESFQVDLGGRYMKINTVEYRSFGVSRSGFYLAFODYGCMSLIIVRFY 180
QY 181 RKCPRIIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEWLVPICRC 240
Db 181 RKCPRIIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEWLVPICRC 240
QY 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSECATNCVCNRYRADL 300
Db 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSECATNCVCNRYRADL 300
QY 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
QY 361 CGDNVOYAPROLGLEPRITVYISDLAHTQYFEIOAVNGVYDQSPFSQFASVNTTNOA 420
Db 361 CGDNVOYAPROLGLEPRITVYISDLAHTQYFEIOAVNGVYDQSPFSQFASVNTTNOA 420
QY 421 APSAVSIHMOYSRIVDSITLISWSOPDQNGVILDELOYYEKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIHMOYSRIVDSITLISWSOPDQNGVILDELOYYEKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYFQVRAATVAGYRGYSKMYEQMTAEVQTSIOEKPLILIGSSAGLVFLI 540
Db 481 GLKAGAIYFQVRAATVAGYRGYSKMYEQMTAEVQTSIOEKPLILIGSSAGLVFLI 540
QY 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVEFAKEI 600
Db 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVEFAKEI 600
QY 601 DISCVKIEOVYAGGEFEGVCSGHLKLPGRKEIFAATILKSGYTEKORRDFLSASIMQ 660
Db 601 DISCVKIEOVYAGGEFEGVCSGHLKLPGRKEIFAATILKSGYTEKORRDFLSASIMQ 660
QY 661 FDHENVHLEBGVYKSTPVMITTEFMENGSLDSPLRONDQFVIOVGMRLGIAGMKY 720
Db 661 FDHENVHLEBGVYKSTPVMITTEFMENGSLDSPLRONDQFVIOVGMRLGIAGMKY 720
QY 721 LADMNYVHRLAARNILVNSNLVKVSDFGLSRLEDDTSDPTYTSLGKFPRIWTAPE 780
Db 721 LADMNYVHRLAARNILVNSNLVKVSDFGLSRLEDDTSDPTYTSLGKFPRIWTAPE 780
QY 781 AIORYKFTSASDVWSYGIWMEVMSYGERPYMDTNDVYNAIEODYRLPMPDCSALH 840
Db 781 AIORYKFTSASDVWSYGIWMEVMSYGERPYMDTNDVYNAIEODYRLPMPDCSALH 840
QY 841 QLMIDCWOKDRNHRPKFGQIVNTLDKMRNPSLKAMAPLSSGINDPLDRTIPDTSFN 900
Db 841 QLMIDCWOKDRNHRPKFGQIVNTLDKMRNPSLKAMAPLSSGINDPLDRTIPDTSFN 900
QY 901 TYDEMLEAIKMGYKESFANAGTSEFVYSOMMEDILRVGVTLAGHOKILINSIOVMA 960
Db 901 TYDEMLEAIKMGYKESFANAGTSEFVYSOMMEDILRVGVTLAGHOKILINSIOVMA 960
QY 961 QMNOIOSVEY 970
Db 961 QMNOIOSVEY 970

```

RESULT 2  
 US-08-702-367A-11  
 : Sequence 11, Application US/08702367A  
 : Patent No. 5981246

GENERAL INFORMATION:  
 APPLICANT: Fox, Gary M.  
 TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
 : Kinases  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Patent Operations/RBW  
 STREET: 1840 Dehaven Drive  
 CITY: Thousand Oaks

```

STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-367A-11

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Query Match 100.0%; Score 5116; DB 2; Length 970;

Best local Similarity 100.0%; Pred. No. 0; Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LLAABETLMDSTTAAELGMVHPSPSGWEVSGVDENNNTIRTYOVNVPSSONMLR 60
Db 1 LLAABETLMDSTTAAELGMVHPSPSGWEVSGVDENNNTIRTYOVNVPSSONMLR 60
QY 61 TKFIRRGARHRIHVEKFSVRDCCSLPSVPGCKEFTFNLYYEADPDSKTKFFPMMEHP 120
Db 61 TKFIRRGARHRIHVEKFSVRDCCSLPSVPGCKEFTFNLYYEADPDSKTKFFPMMEHP 120
QY 121 WKVDTIADESFQVDLGGRYMKINTVEYRSFGVSRSGFYLAFODYGCMSLIIVRFY 180
Db 121 WKVDTIADESFQVDLGGRYMKINTVEYRSFGVSRSGFYLAFODYGCMSLIIVRFY 180
QY 181 RKCPRIIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEWLVPICRC 240
Db 181 RKCPRIIIONGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDDEWLVPICRC 240
QY 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSECATNCVCNRYRADL 300
Db 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSECATNCVCNRYRADL 300
QY 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
QY 361 CGDNVOYAPROLGLEPRITVYISDLAHTQYFEIOAVNGVYDQSPFSQFASVNTTNOA 420
Db 361 CGDNVOYAPROLGLEPRITVYISDLAHTQYFEIOAVNGVYDQSPFSQFASVNTTNOA 420
QY 421 APSAVSIHMOYSRIVDSITLISWSOPDQNGVILDELOYYEKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIHMOYSRIVDSITLISWSOPDQNGVILDELOYYEKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYFQVRAATVAGYRGYSKMYEQMTAEVQTSIOEKPLILIGSSAGLVFLI 540
Db 481 GLKAGAIYFQVRAATVAGYRGYSKMYEQMTAEVQTSIOEKPLILIGSSAGLVFLI 540
QY 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVEFAKEI 600
Db 541 AVVVAIYVNCNRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNAVEFAKEI 600
QY 601 DISCVKIEOVYAGGEFEGVCSGHLKLPGRKEIFAATILKSGYTEKORRDFLSASIMQ 660
Db 601 DISCVKIEOVYAGGEFEGVCSGHLKLPGRKEIFAATILKSGYTEKORRDFLSASIMQ 660
QY 661 FDHENVHLEBGVYKSTPVMITTEFMENGSLDSPLRONDQFVIOVGMRLGIAGMKY 720

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Db 661 FDHPNVTHLEGVYTKSTFVMTTEFMENGSLDSFLRQDQGFVYIOVLGMLGIAAGMY 720
Qy 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSPPTYSALGKFPRTAPE 780
Db 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSPPTYSALGKFPRTAPE 780
Qy 781 AIOYRKFTSASDVWSYGVYVMEVMSYGERPYMDTNDVINAIEODYRLPPMDCPALH 840
Db 781 AIOYRKFTSASDVWSYGVYVMEVMSYGERPYMDTNDVINAIEODYRLPPMDCPALH 840
Qy 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRPNLSLKAMAPLSSGINTPLDRTIPDTSFN 900
Db 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRPNLSLKAMAPLSSGINTPLDRTIPDTSFN 900
Qy 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSOMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Db 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSOMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Qy 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

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RESULT 3
PCT-US95-04681-11
; Sequence 11, Application PC/TUS9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Amgen Patent Operations/RBM
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04681
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04681-11

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Query Match 100.0%; Score 5116; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LAAVEETLMSSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVCNVESSQNMWLR 60
Db 1 LAAVEETLMSSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVCNVESSQNMWLR 60
Qy 61 TKETRRRAAHIIHYEMKFSVSDSSIPSPGCKETFNLLYYEADFDSATKTFPNMME 120
Db 61 TKETRRRAAHIIHYEMKFSVSDSSIPSPGCKETFNLLYYEADFDSATKTFPNMME 120
Qy 121 WKVDITIADESQVDLGRVVKINTEVRSFGVSHSGRYLAFQDYGCSMLIAVRVF 180

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Db 121 WKVDITIADESQVDLGRVVKINTEVRSFGVSHSGRYLAFQDYGCSMLIAVRVF 180
Qy 181 RCPRIITONGALFOETLSAESTSLVAARGSCIANAEEDVPITKYCGDDEMLVPIGR 240
Db 181 RCPRIITONGALFOETLSAESTSLVAARGSCIANAEEDVPITKYCGDDEMLVPIGR 240
Qy 241 MCKAGEAVENTVRCGPGSGTFKANOGEACTHCPIINSRTTSEGATNCVCNRYRADL 300
Db 241 MCKAGEAVENTVRCGPGSGTFKANOGEACTHCPIINSRTTSEGATNCVCNRYRADL 300
Qy 301 DPLDMPCCTTIPSAPOAVISSVNETSLMLEMTPPRRSGREDLVYNIITCKSCSGRGACTR 360
Db 301 DPLDMPCCTTIPSAPOAVISSVNETSLMLEMTPPRRSGREDLVYNIITCKSCSGRGACTR 360
Qy 361 CGDNQOYAPROLGLTEPRITYSIDLAAHTQYTFEIOAVNGVTDQSPSPFASVITNOA 420
Db 361 CGDNQOYAPROLGLTEPRITYSIDLAAHTQYTFEIOAVNGVTDQSPSPFASVITNOA 420
Qy 421 APSAVSIMHOVSRTYDSTTSLMSQPDQNGYILDYELQYEBELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHOVSRTYDSTTSLMSQPDQNGYILDYELQYEBELSEYNATAIKSPNTVT 480
Qy 481 GLKAGAIYFQVRAVYAGYGRYSGKMYFQMTPEAYOTSIOEKLPLITGSSAAGVFLI 540
Db 481 GLKAGAIYFQVRAVYAGYGRYSGKMYFQMTPEAYOTSIOEKLPLITGSSAAGVFLI 540
Qy 541 AVVYAIAYCNRRGERADSETYDLOHTSGHTPGKKIYIDPPTYBDPEAVREFAKEL 600
Db 541 AVVYAIAYCNRRGERADSETYDLOHTSGHTPGKKIYIDPPTYBDPEAVREFAKEL 600
Qy 601 DISCVKIEOVGAGEFGEVCSGHILKPGKREIFAIKTLKSGYTEORRPFLEASIMGO 660
Db 601 DISCVKIEOVGAGEFGEVCSGHILKPGKREIFAIKTLKSGYTEORRPFLEASIMGO 660
Qy 661 FDHPNVTHLEGVYTKSTFVMTTEFMENGSLDSFLRQDQGFVYIOVLGMLGIAAGMY 720
Db 661 FDHPNVTHLEGVYTKSTFVMTTEFMENGSLDSFLRQDQGFVYIOVLGMLGIAAGMY 720
Qy 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSPPTYSALGKFPRTAPE 780
Db 721 LADNMYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSPPTYSALGKFPRTAPE 780
Qy 781 AIOYRKFTSASDVWSYGVYVMEVMSYGERPYMDTNDVINAIEODYRLPPMDCPALH 840
Db 781 AIOYRKFTSASDVWSYGVYVMEVMSYGERPYMDTNDVINAIEODYRLPPMDCPALH 840
Qy 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRPNLSLKAMAPLSSGINTPLDRTIPDTSFN 900
Db 841 QLMIDCQOKDRNHRPKFGQIVNTLDKMIIRPNLSLKAMAPLSSGINTPLDRTIPDTSFN 900
Qy 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSOMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Db 901 TVDWMLEAIKMGQYKESFANAGFTSFVVSOMMEDILRVGVTLAGHOKKILNSIOVMRA 960
Qy 961 QMNOIOSVEV 970
Db 961 QMNOIOSVEV 970

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RESULT 4
US-08-542-635-2
; Sequence 2, Application US/08542635
; Patent No. 6218356
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; APPLICANT: Letwin, Kenneth
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Bereskin & Parr

```

STREET: 40 King Street West, Box 401  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5H 3Y2  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/542,635  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McDiarmid, Shona S.  
 REGISTRATION NUMBER: 38,798  
 REFERENCE/DOCKET NUMBER: 3153-162  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 364-7311  
 TELEFAX: (416) 361-1398  
 TELEX: 06-23115  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 994 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Mus musculus  
 DEVELOPMENTAL STAGE: Embryo  
 IMMEDIATE SOURCE:  
 LIBRARY: lambda gt10 cDNA library  
 CLONE: Combined pNKRACE A2 and K2 and cDNA clones  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: Distal end of chromosome 4  
 MAP POSITION: near the ahd-1 mutation  
 US-08-542-635-2

Query Match 99.3%; Score 5082; DB 4; Length 994;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 1 ILAAVEETLMDSTATAELGWMVHPSPGMEVSGIDEMNTIRITYQVNCVNESSQNMWLR 60  
 DB 23 ILAAVEETLMDSTATAELGWMVHPSPGMEVSGIDEMNTIRITYQVNCVNESSQNMWLR 82  
 QY 61 TFFIRRGHRIHVEMKFSVRDCSSIPVPGSKETFNLYYYEADFDSATKTFPMWENP 120  
 DB 83 TFFIRRGHRIHVEMKFSVRDCSSIPVPGSKETFNLYYYEADFDLATTFPMWENP 142  
 QY 121 WKVVDTIADSEFSQVDLGRVYKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRFY 180  
 DB 143 WKVVDTIADSEFSQVDLGRVYKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRFY 202  
 QY 181 RKCPRITONGAIFQETLSAESTSLVAARGSCIANAEEDVPIKLYCGDGEMLVPIGRG 240  
 DB 203 RKCPRITONGAIFQETLSAESTSLVAARGSCIANAEEDVPIKLYCGDGEMLVPIGRG 262  
 QY 241 MCKAGEAENGVCGCGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300  
 DB 263 MCKAGEAENGVCGCGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322  
 QY 301 DPLDMCTTIPSAQAVISSVNETSLMEWTPPPROSGGREDLVYNTICKSCSGGACACTR 360  
 DB 323 DPLDMCTTIPSAQAVISSVNETSLMEWTPPPROSGGREDLVYNTICKSCSGGACACTR 382  
 QY 361 CGNNVYARQGLGTEPRYISDLAHQYTFEIOAVNCVQSPSPQFASVNTITNQA 420  
 DB 383 CGNNVYARQGLGTEPRYISDLAHQYTFEIOAVNCVQSPSPQFASVNTITNQA 442

QY 421 APSAVSIMHOVSRTVDSITLMSQPDQPNVILIDYELQYEEKELSEXNATAIKSPNTNVT 480  
 DB 443 APSAVSIMHOVSRTVDSITLMSQPDQPNVILIDYELQYEEKELSEXNATAIKSPNTNVT 502  
 QY 481 --GLKAGAIYFQYARATVAGYGRYSGRMVFQYMTAEAYQTSIOEKPLIIGSSAGLVF 538  
 DB 503 VQGLKAGAIYFQYARATVAGYGRYSGRMVFQYMTAEAYQTSIOEKPLIIGSSAGLVF 562  
 QY 539 LIAVVIAIVCNRRGFERADEYTDKLOHTYSGHITGMYKIDPFYEEDPNEAVREFAK 598  
 DB 563 LIAVVIAIVCNRRGFERADEYTDKLOHTYSGHITGMYKIDPFYEEDPNEAVREFAK 622  
 QY 599 EIDISCYKIEOVYIGAGEFEGSCGHLKPGKREIFVAIKTLKSGYTEKORDFLEASIM 658  
 DB 623 EIDISCYKIEOVYIGAGEFEGSCGHLKPGKREIFVAIKTLKSGYTEKORDFLEASIM 682  
 QY 659 GGFDPNVYHLEGVYTKSTPMVITTEFMENGLSDSFLRQNDGQTVYQVGMRLGIAAG 718  
 DB 683 GGFDPNVYHLEGVYTKSTPMVITTEFMENGLSDSFLRQNDGQTVYQVGMRLGIAAG 742  
 QY 719 KYLADMNYYHRLARNTLVNSNLVCKYSDGSLREFLEDOTSDPTYSALGKFPIMTA 778  
 DB 743 KYLADMNYYHRLARNTLVNSNLVCKYSDGSLREFLEDOTSDPTYSALGKFPIMTA 802  
 QY 779 PEAIQYRKFTSADVKSQYGIYVMEVMSYGERPYMDTNOVYINAEIDYRLPPMDCPSA 838  
 DB 803 PEAIQYRKFTSADVKSQYGIYVMEVMSYGERPYMDTNOVYINAEIDYRLPPMDCPSA 862  
 QY 839 LHQMLDCKOKRNRHPRKGOIVNTLDKMRNPNSLKMAPLSSGINPLDRTIPDVT 898  
 DB 863 LHQMLDCKOKRNRHPRKGOIVNTLDKMRNPNSLKMAPLSSGINPLDRTIPDVT 922  
 QY 899 FNVVDEMLAIKMGQYKESFANAGFTSPDYVSQMMEDILRVGVTLAHOXKILINSIOV 958  
 DB 923 FNVVDEMLAIKMGQYKESFANAGFTSPDYVSQMMEDILRVGVTLAHOXKILINSIOV 982  
 QY 959 RAQMNQIOSVEV 970  
 DB 983 RAQMNQIOSVEV 994

RESULT 5  
 US-08-162-809-18  
 ; Sequence 18, Application US/08162809  
 ; Patent No. 5457048  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pasquale, Elena B.  
 ; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CAMPBELL AND FLORES  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; City: San Diego  
 ; STATE: California  
 ; COUNTRY: United States of America  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/162,809  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; REFERENCE/DOCKET NUMBER: P-LJ 9503  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 995 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-162-809-18

Query Match 96.8%; Score 4950.5; DB 1; Length 995;  
 Best Local Similarity 95.6%; Pred. No. 0;  
 Matches 930; Conservative 28; Mismatches 12; Indels 3; Gaps 2;

QY 1 LLAAVEETLMDSTTATATLGMVHPSPGMEVSGYDENMNTIRTYOVQCNVFESSONMMLR 60  
 DB 23 LLAAVEETLMDSTTATATLGMVHPSPGMEVSGYDENMNTIRTYOVQCNVFESSONMMLR 82  
 QY 61 TKFTRRGARHRIHVEKMFVSDCSSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 120  
 DB 83 TKYIRRGARHRIHVEKMFVSDCSSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 142  
 QY 121 WVKVDITIADESFQVDLGGRVKINTEVRSFGVSRSGFYLAFODYGGCSLIAVRVY 180  
 DB 143 WVKVDITIADESFQVDLGGRVKINTEVRSFGVSRSGFYLAFODYGGCSLIAVRVY 202  
 QY 181 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLXNGDEWLVPIGRC 240  
 DB 203 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLXNGDEWLVPIGRC 262  
 QY 241 MCKAGFEAVENGTVCRGCPSGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGYRDL 300  
 DB 263 MCKAGFEAVENGTVCRGCPSGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGYRDL 322  
 QY 301 DPLDMOCTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNTICKSCSGRGACTR 360  
 DB 323 DPLDMOCTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNTICKSCSGRGACTR 382  
 QY 361 CGDNVOYAPROGLTEPRRIYISDLAHTOYFEOIAVNVQDOSPSPQAFANVTITNOA 420  
 DB 383 CGDNVOYAPROGLTEPRRIYISDLAHTOYFEOIAVNVQDOSPSPQAFANVTITNOA 442  
 QY 421 APSAVSIMQVSTVDSTLSWSODPQNGVILDELOYEKELESEYNTAISKSPNTVT 480  
 DB 443 APSAVSIMQVSTVDSTLSWSODPQNGVILDELOYEKELESEYNTAISKSPNTVT 502  
 QY 481 --GLKAGAIYFQVRRATVAGYGRYSGKMYRQTMTEAEVQTSIQEKLIISSAAGLVF 538  
 DB 503 VONLKAGTIYVQVARRATVAGYGRYSGKMYRQTMTEAEVQTSIQEKLIISSAAGLVF 562  
 QY 539 LIAVVYIAIVCN-RRGFERADSEYTDKLOHTYSGHITPGMKIYIDPFTYEDPNEAVREFA 597  
 DB 563 LIAVVYIAIVCN-RRGFERADSEYTDKLOHTYSGHITPGMKIYIDPFTYEDPNEAVREFA 622  
 QY 598 KEIDISCVIIEVOVIGAGEGVCCHLTKPKGREIFVAIKTLKSGYTERKQRDLSEASI 657  
 DB 623 KEIDISCVIIEVOVIGAGEGVCCHLTKPKGREIFVAIKTLKSGYTERKQRDLSEASI 682  
 QY 658 MGFDPHNVIIHLEGVYVSTPVMITTEFMENGSLDSFLRQNDQFITYIQLVGMRLGRTAG 717  
 DB 683 MGFDPHNVIIHLEGVYVSTPVMITTEFMENGSLDSFLRQNDQFITYIQLVGMRLGRTAG 742  
 QY 718 MKYLLDMNVVIRDLAARILVNSNLVCVSPFGLSRFLEDDTSDPTYSALGKFRIRMT 777  
 DB 743 MKYLLDMNVVIRDLAARILVNSNLVCVSPFGLSRFLEDDTSDPTYSALGKFRIRMT 802  
 QY 778 APEALQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNOOVINAITODVRLPRMPCPS 837  
 DB 803 APEALQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNOOVINAITODVRLPRMPCPS 862  
 QY 838 ALHQLMLDCKQKORNRHPRKFGQIYNTLDKMIIRNPNSLKANAPLSSGILNPLDLRTTIPDY 897  
 DB 863 ALHQLMLDCKQKORNRHPRKFGQIYNTLDKMIIRNPNSLKANAPLSSGILNPLDLRTTIPDY 922

QY 898 SFNTVDEMLDAIKMQYKESFANAGFTSPDVVSOMMEDILRVGTLAGHOKKILNSIQV 957  
 DB 923 SFNTVDEMLDAIKMQYKESFANAGFTSPDVVSOMMEDILRVGTLAGHOKKILNSIQV 982  
 QY 958 MRAQNMQIOSVEY 970  
 DB 983 MRAQNMQIOSVEY 995

RESULT 6  
 US-08-162-809-12  
 Sequence 12, Application us/08162809  
 Patent No. 5457048  
 GENERAL INFORMATION:  
 APPLICANT: Pasquale, Elena B.  
 APPLICANT: Sajjad, Fereydoon G.  
 TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL AND FLORES  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/162, 809  
 FILING DATE:  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LJ 9503  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1011 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-162-809-12

Query Match 96.5%; Score 4934.5; DB 1; Length 1011;  
 Best Local Similarity 94.0%; Pred. No. 0;  
 Matches 930; Conservative 28; Mismatches 12; Indels 19; Gaps 3;

QY 1 LLAAVEETLMDSTTATATLGMVHPSPGMEVSGYDENMNTIRTYOVQCNVFESSONMMLR 60  
 DB 23 LLAAVEETLMDSTTATATLGMVHPSPGMEVSGYDENMNTIRTYOVQCNVFESSONMMLR 82  
 QY 61 TKFTRRGARHRIHVEKMFVSDCSSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 120  
 DB 83 TKYIRRGARHRIHVEKMFVSDCSSIPVSGCKETFNLYYEADPDSATKTFPMNMENP 142  
 QY 121 WVKVDITIADESFQVDLGGRVKINTEVRSFGVSRSGFYLAFODYGGCSLIAVRVY 180  
 DB 143 WVKVDITIADESFQVDLGGRVKINTEVRSFGVSRSGFYLAFODYGGCSLIAVRVY 202  
 QY 181 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLXNGDEWLVPIGRC 240  
 DB 203 RKCPRIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLXNGDEWLVPIGRC 262  
 QY 241 MCKAGFEAVENGTVCRGCPSGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGYRDL 300

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MEDUITYTYPE: FLOPEY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673.789
FILING DATE:
CLASSIFICATION: 4:5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177, 812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPEL
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 754-6849
TELEX: 421/92
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 995
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
US-08-673-789-5

Query Match      96.2%; Score 4919.5; DB 2; Length 995;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 923; Conservative 30; Mismatches 17; Indels 3; Gaps 2

OY 1 LLAEEETLMDSTATAELGMMVHPSPGMBEYSGVDENMNTIRTYOVGNFPSSQNMMLR 60
    |||
DB 23 LLAEEETLMDSTATAELGMMVHPSPGMBEYSGVDENMNTIRTYOVCKVESSQNMMLR 82
    |||

OY 61 TKFIRRGAAHRIHEMFEFSVRDCSSIPSPVSGCKETENLYYEADFDSATRTFPMHMEP 120
    |||
DB 83 TKYIRRAAHRIHEMFEFSVRDCSSIPNVSCKETFNLYYESDFDSTATFPMHMEP 142
    |||

OY 121 WKVDTTAADESFQVDLGRVWKINTEVPSRGSFYLAFODYGCKMSLLAVREY 180
    |||
DB 143 WKRVDTTAADESFQVDLGRVWKINTEVPSRGSFYLAFODYGCKMSLLAVREY 202
    |||

OY 181 RKCPRITONGAIFQETLSGAESTSLVANGSCITANAEVDVPIKLYCGDGBMLVPIGR 240
    |||
DB 203 RKCPRITONGAIFQETLSGAESTSLVANGSCITANAEVDVPIKLYCGDGBMLVPIGR 262
    |||

OY 241 MCKAGEFAVENGTVCRCPCSTFEKANGDCHCPINRSRTSEGNATVCNNGYRRADL 300
    |||
DB 263 MCRPGESVENGTVCRCPCSTFEKANGDCHCPINRSRTSEGNATVCNNGYRRADL 322
    |||

OY 301 DPLDMPCTTIPAPPAVATSSVNETSLMLEWTPPRDSGSGREDLYNNICKSCGSGGACTR 360
    |||
DB 323 DPLDMPCTTIPAPPAVATSSVNETSLMLEWTPPRDSGSGREDLYNNICKSCGSGGACTR 382
    |||

OY 361 CGDNVOYARQLGLTEPRITVYISDLIAHTQYTFELQAVNGTLDSPSPQFASVNTTMOA 420
    |||
DB 383 CGDNVOYARQLGLTEPRITVYISDLIAHTQYTFELQAVNGTLDSPSPQFASVNTTMOA 442
    |||

OY 421 APSAVSIMOVSRATVDSITLSMSOPDONGVILDEYELQYEEKLSEYNATAIKSPTNTVT 480
    |||
DB 443 APSAVSIMOVSRATVDSITLSMSOPDONGVILDEYELQYEEKLSEYNATAIKSPTNTVT 502
    |||

OY 481 --GLAKGATVYEQVARNATVAGYGRYSGMATQYMTAEYOTSIQEKPLPLITSSAAGLVF 538
    |||
DB 503 VQMLKAGTIVYEQVARNATVAGYGRYSGMATQYMTAEYOTSIQEKPLPLITSSAAGLVF 562
    |||

OY 539 LIAVVAIATVNC-RKQFERADSEYTDKLOHTTSGHITPPGKKIYIDFTYEDDPNEAVREFA 597
    |||
DB 563 LIAVVAIATVNCRRQFERADSEYTDKLOHTTSGHITPPGKKIYIDFTYEDDPNEAVREFA 622
    |||

OY 598 KEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFAIAIKTLASGTEKORDFPLESAI 657
    |||

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Db 623 KEIDISCVKIQVIGAGEFGEVCGSHLKLPGKREIFAIRTKLKGTYENKGRDPLSLASI 682
Qy 658 MGOEDHPNVHLLEGVYTKSTPVMITTEPFMENGSLDSFLRNDQOFTYIQLVGMRLGIAG 717
Db 683 MGOEDHPNVHLLEGVYTKSTPVMITTEPFMENGSLDSFLRNDQOFTYIQLVGMRLGIAG 742
Qy 718 MKYLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPTYSALGSKFPIRMT 777
Db 743 MKYLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPTYSALGSKFPIRMT 802
Qy 778 APEAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPN 837
Db 803 APEAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPN 862
Qy 838 ALHQLMDCQKORNRHPRKFGQIVNTLDKMIKRNPNLSLKAAAPLSSGINLPIDRTIPDT 897
Db 863 ALHQLMDCQKORNRHPRKFGQIVNTLDKMIKRNPNLSLKAAAPLSSGINLPIDRTIPDT 922
Qy 898 SFNTVDEMLAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTLGAGHOKKILNSIOY 957
Db 923 SFNTVDEMLAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTLGAGHOKKILNSIOY 982
Qy 958 MRAQNMQIOSVEY 970
Db 983 MRAQNMQIOSVEY 995

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RESULT 8
US-08-673-789-6
Sequence 6, Application US/08673789
Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, REMPING; SCHULZ, NICHOLAS.
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 984
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN

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; TOPOLOGY: UNKNOWN
US-08-673-789-6

Query Match 76.4% Score 3909.5; DB 2; Length 984;
Best Local Similarity 73.9% Pred. No. 1,7e-290;
Matches 716; Conservative 128; Mismatches 122; Indels 3; Gaps 2;

Qy 2 LAABETLMDSTTAETAEELGMVHPSPGSEEVSGYDENMNTTRTQOVNVESSONMLRT 61
Db 15 VAAMEETLMDSTRITAEELGMVHPSPGSEEVSGYDENMNTTRTQOVNVESSONMLRT 74
Qy 62 KFIIRRGARHRIHVEMKTSVRDCSSIPSPGSCETFMILYYEADFSDATKTFPMMEHP 121
Db 75 TFINRGARHRIYTEMRFTRVDCSSLPVNPVPGSKETFMILYYEADFSDATKTFPMMEHP 134
Qy 122 VKVDITADESFQVODLGGRYMKINTEVRSGPVSRSRGFLAODVGGCSLAVRVPFR 181
Db 135 LKVDTIADESFQVODLGGRYMKINTEVRSGPVSRSRGFLAODVGGCSLAVRVPFR 194
Qy 182 KCPRIQNGAIEOETLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDEMLVPIGRCM 241
Db 195 KCPRIQNGAIEOETLSGAESTSLVAARGSCIANAEEDVPIKLYCNGDEMLVPIGRCM 254
Qy 242 CKAGEAENGTVCRGCGPSTGFEKANGODEACTHCPIINSRTSGCATNCYCRNGYRADLD 301
Db 255 CKAGEAENGTVCRGCGPSTGFEKANGODEACTHCPIINSRTSGCATNCYCRNGYRADLD 313
Qy 302 PLDNPCTTIPSAQAVISSVNETSLMLEWPPRDSGREDLVNIIKCGSGGRACCTRC 361
Db 314 PPEVACTSVSPGRNVIISVNETSLMLEWPPRDSGREDLVNIIKCGSGGRACCTRC 373
Qy 362 GDNVQVAPRDLGTERITISDLANTOYFETIQAVNGVTDOSPESPOFASVNTITNQA 421
Db 374 DNVQVAPRDLGTERITISDLANTOYFETIQAVNGVTDOSPESPOFASVNTITNQA 433
Qy 422 PSAVSIHQVSRVDSITLSMSQDOPNGVILDELOYEKELSEVNTAISPTNT--V 479
Db 434 PSTVPIHQVSRVDSITLSMSQDOPNGVILDELOYEKELSEVNTAISPTNT--V 493
Qy 480 TGLKAGAIYFOVRAITVAGYGRYSGMYFOYMTAEVOTSIOEKPLITIGSSAAGLVFL 539
Db 494 DGLRPMGVYVVOVRAITVAGYGRYSGMYFOYMTAEVOTSIOEKPLITIGSSAAGLVFL 553
Qy 540 IAAVVAIYCNRRGEFRADEYTDKLOHTSGHITTPGAKITIDPTTYEDPNEAREFAKE 599
Db 554 VSLVAISIVCSKRRAYSKAIVYSDKLOHTSGHITTPGAKITIDPTTYEDPNEAREFAKE 613
Qy 600 IDISCVKIQVIGAGEFGEVCGSHLKLPGKREIFAIRTKLKGTYENKGRDPLSLASI 659
Db 614 IDISCVKIQVIGAGEFGEVCGSHLKLPGKREIFAIRTKLKGTYENKGRDPLSLASI 673
Qy 660 OFDHPNVHLLEGVYTKSTPVMITTEPFMENGSLDSFLRNDQOFTYIQLVGMRLGIAG 719
Db 674 OFDHPNVHLLEGVYTKSTPVMITTEPFMENGSLDSFLRNDQOFTYIQLVGMRLGIAG 733
Qy 720 YLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPTYSALGSKFPIRMT 779
Db 734 YLADNMVYHRLDAARNILVNSNLVCKVSDFGLSRLEDDTSDPTYSALGSKFPIRMT 793
Qy 780 APEAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPN 839
Db 794 APEAIORRKTFSASDVWSYGIWMEVWSYGERPYWMTNODVYNAIEODYRLPPMDCPN 853
Qy 840 HOLMIDCQKORNRHPRKFGQIVNTLDKMIKRNPNLSLKAAAPLSSGINLPIDRTIPDT 899
Db 854 HOLMIDCQKORNRHPRKFGQIVNTLDKMIKRNPNLSLKAAAPLSSGINLPIDRTIPDT 913
Qy 900 NTVDMLAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTLGAGHOKKILNSIOY 959
Db 914 NTVDMLAIKMGQYKESFANAGTSPEDVVSQMMEDILRAGVTLGAGHOKKILNSIOY 973
Qy 960 AQNMQIOSV 984

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Db 974 VQNMOSPSV 982

# RESULT 9

US-08-162-809-2  
Sequence 2, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 951 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-809-2

Query Match 72.4%; Score 3706.5; DB 1; Length 951;  
Best Local Similarity 70.2%; Pred. No. 5.2e-275;  
Matches 687; Conservative 120; Mismatches 117; Indels 55; Gaps 4;

Db 7 ETLMDSTATAELGMMVHPGSGMEVSGYDGMNTRTYQVCNVPESONMLRTKFTIR 66  
1 ETLMDSTATAELGMMVHPGSGMEVSGYDGMNTRTYQVCNVPESONMLRTKFTIR 60  
67 RGAHRIVHMKRVSVDSSIPVSGCKETFNLYYEADFDSATKTFPMNENPVKVDY 126  
61 RGAHRIVHMKRVSVDSSIPVSGCKETFNLYYEADFDSATKTFPMNENPVKVDY 120  
127 IAADESFQVDLGRVYKINTEVRSFGVSRSGFLAODYGGCMLAARVFKCPRI 186  
121 IAADESFQVDLGRVYKINTEVRSFGVSRSGFLAODYGGCMLAARVFKCPRI 147  
187 IONGALFOTLSAESTSVAAAGSCIANAEVDYPIKLYCNGDEMLVPIGRCKAGF 246  
148 VONFALEPMTGAESTSVTAAGTIPPAEVDYPIKLYCNGDEMLVPIGRCKAGF 207  
247 EAVENGTVRCGSPGTFKANOGDEACTHCPINSRTSGATNCVCNRYRADLPLDMP 306  
208 EP-ENNACACAGAGTFKASOGAGLCARCPNRSASAEASPLACACNGYERADLPPTAA 266  
307 CTIIPSAQAVISSVNETSILEMTTPRDSGGEDLVYNIICKSGCGACRCGDVNO 366  
267 CTVPSPGPRNVIVISVETSIILEMNPRTGTGDDVYINICKKCRADYRACRCDDNVE 326

QY 367 YAPROGLTEPRIVISDLAHOTPELQAVNGVTDSPPQFASANTITNOAPSAYS 426  
Db 327 FVPROGLTEPRIVISDLAHOTPELQAVNGVTDSPPQFASANTITNOAPSAYS 386  
QY 427 IMHOVSRTVDSITLSMSQPOPNVILDEYOYER-----ELSEY 467  
Db 387 IMHOVSRTVDSITLSMSQPOPNVILDEYOYER-----ELSEY 446  
QY 468 NATAKSPNT-VTGLKAGATVYQVARTVAGYGSCKMFORMTEAEYOTSIOEKI 525  
Db 447 NSSVARSQNTARLEGLRPGVWYVQVARTVAGYGSCKMFORMTEAEYOTSIOEKI 506  
QY 526 PLIIGSSAGIVFLAVVAIVAVICNRRGFERADEYDKLOHYTSGHITPGMKYIDPFT 585  
Db 507 PLIIGSSAGIVFLAVVAIVAVICNRRGFERADEYDKLOHYTSGHITPGMKYIDPFT 566  
QY 586 YEDPNEAVREPAKEILISCVKIEOVIGAGEFGEVCSGHLKIPKRELFVAIKLKSQTE 645  
Db 567 YEDPNEAVREPAKEILISCVKIEOVIGAGEFGEVCSGHLKIPKRELFVAIKLKSQTE 626  
QY 646 KORDFLSEASIMGOIHPNVIHLEGVYTKSPVMIITEPEMENGSLDPLRONGQFTVI 705  
Db 627 KORDFLSEASIMGOIHPNVIHLEGVYTKSPVMIITEPEMENGSLDPLRONGQFTVI 686  
QY 706 OLVGMLRGIAAGMKYIADNMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDTSPTTY 765  
Db 687 OLVGMLRGIAAGMKYIADNMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDTSPTTY 746  
QY 766 SAIGKFPRTAPENIOTRKETSASDVWSYGIWMEVMSYGERPYDMNTODYINAEQ 825  
Db 747 SSIIGKFPRTAPENIOTRKETSASDVWSYGIWMEVMSYGERPYDMNTODYINAEQ 806  
QY 826 DYRLPPMDCPSALHOLMDCKORNRHPRKFGQIVNTLDMKIRNPUSLKAMAPLSSGIN 885  
Db 807 DYRLPPMDCPSALHOLMDCKORNRHPRKFGQIVNTLDMKIRNPUSLKAMAPLSSGIN 866  
QY 886 LPLDRTIPDYTSFNTVDEMLDAIKMGQYKESFANAGTSPDYVSOMMEIILRGVTLA 945  
Db 867 LPLDRTIPDYTSFNTVDEMLDAIKMGQYKESFANAGTSPDYVSOMMEIILRGVTLA 926  
QY 946 GHOKTILNSTQVRAQMO 964  
Db 927 GHOKTILNSTQVRAQMO 945

## RESULT 10

US-08-162-809-10  
Sequence 10, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESS: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:





196 TISGASTSLVARGSCIANAEVDVPIKLCXNGDSEMIYPIGRCKMKAEGEAVENGTV 255  
197 TITGAPETSLVAPGTCICINAEVSVPLKLYCGDEMMVPGACICAGYEPAKMDTQC 256  
256 RCPSTETFGANDEACTHCPIINSRTSGATNCVCRNGYRRADLPDLPMPCTTIPSAQ 315  
257 QACGPETFKSGEGSCSPCPSPSRRTAGATVCICRSGEFFRADADPADSACSIVSAR 316  
316 AVISSVNETSLMEWTPPRDSGGREDLVYNIICKSCSGRGACTRCGDVNVQVAPRL--- 372  
317 SVISSNETSLVLEWSEPDAGGRDLDLVNYICKCSVERRLCSRDDVNEFPRDGLT 376  
373 GTEPRYISDLAHQYFETIOAVNGVDSPEFOPASVNTTQAAPSAIVHNOVS 432  
377 GLTERIYISKVAHPQYFETIOAVNGISKSFPPEHFSVNTTQAAPSAIVHNLHS 436  
433 RYVDSITLMSQPDQNGVILDELOYEKE--LSEYNATAIKSPNTV--TGKACAIVY 489  
437 STGNSMTLSMTPEPENGILDEYIKSEKQGGDIANTVYSQKNSVRLDGLKANARYM 496  
490 FOYRATVAGYGRYSKMTFQMTTEAYOTSTOEKPLIIGSSAAGVELIAVVAIYC 549  
497 VOYRATVAGYGRYSKMTFQMTTEAYOTSTOEKPLIIGSSAAGVELIAVVAIYC 556  
550 NRRGF-----ERADSEYTDKLOHYTSGHITPGKITYIDPPTYEDPNEAYR 594  
557 FRKGMVTEOLLSPGLRKORNSIDPPEYTERKLOQ---VTPGKAVIYIDPPTYEDPNEAYR 612  
595 EFAKEIDISCVKIEOYIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLE 654  
613 EFAKEIDISCVKIEEYIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLE 672  
655 ASIMGCFDHPNVIHLEGVYTKSTPVMITTEFEMNGSLDSTLRNDQGFYIOLVGMRLGI 714  
673 ASIMGCFDHPNVIHLEGVYTKSTPVMITTEFEMNGSLDSTLRNDQGFYIOLVGMRLGI 732  
715 AAGMKTLADNMYHRLDAAARNILVNSNLCKVSDFGLSRLEDSDPPTYTSALGKFP 774  
733 AAGMKTLSENNYHRLDAAARNILVNSNLCKVSDFGLSRLEDSDPPTYTSALGKFP 792  
775 RMTAPAIORRKTSSASDVSYGIVMEVWSYGERPYMDTNOVINAIEODYRLPEPMD 834  
793 RMTAPAIARKTSSASDVSYGIVMEVWSYGERPYMDTNOVINAIEODYRLPEPMD 852  
835 CPBALHQLMDCKQRNHRPKQIYVNLDKIRMPNSLKAAAPLSSGINPLDRTIP 894  
853 CPBALHQLMDCKQRNHRPKQIYVNLDKIRMPNSLKAAAPLSSGINPLDRTIP 912  
895 DYSFNTVEMLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRYGVTLAGHOKILNS 954  
913 DYTFTTVGDMDLAIKMGYKESFANAGFTSPDVVSQMMEDILRYGVTLAGHOKILNS 972  
955 IOVRAOMNOIOSVEY 970  
973 IODMRLQMLTPEVQY 988

RESULT 12  
US-08-449-645A-20  
; Sequence 20, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBM  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,645A  
FILING DATE:  
CLASSIFICATION: 4:5  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-449-645A-20

Query Match 71.0%; Score 3632.5; DB 2; Length 998;  
Best Local Similarity 70.5%; Pred. No. 2.6e-269;  
Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

4 AVEETLMDSTTAEIAGMVAHPSPGSEVSGYDENNTIRTYOVGVNFESSONNMLRTE 63  
1 AVEETLMDSTTAEIAGMVAHPSPGSEVSGYDENNTIRTYOVGVNFESSONNMLRTE 63  
37 ALEETLMDKRWTSSELAMVSHPSGSEVSGYDEANPRTYQVNCVNRSSONNMLRTGE 96  
64 IRRGARHIVHEKFEIVRCCSIPSVGCKETFNLYYEADFDASATKTFPMNMENPVK 123  
97 IMRDQYRYVELKFTVYRONSIPNPGCKETFNLFYEADSDVASASSPMMENPVYK 156  
124 VDTIADESFOYDLGRYMKINTYEVRSFPVRSRGTFLAFODYGGCMLIAVRYRKC 183  
157 VDTIADESFSRLDA---RVNTKVRSEGPLSKAGFYLAFODOGCMSLISVRAFYKC 212  
184 PRIOGATFOETLSGAESESLVAARGSCIANAEVDVPIKLYCNGDSEMIYPIGRCKM 243  
213 ASTTAGFALPELTGAEFTSLVIAFGTCIPNAVEVSVPLKLYCNGDSEMIYPIGRCKM 272  
244 AGEAVENGTVCGCHSGTFKCANOGDEACTHCPINSRTSGATNCVCRNGYRRADLP 303  
273 TGEHAPAKSQCPGPGYKAKOGEGPCLPCPPNSRTSPASICTCHNNEFYRADSDSA 332  
304 DMECTTIPAPQAVISSVNETSLMEWTPPRDSGGREDLVYNIICKSC--GSGRGACTRC 361  
333 DSACTTIPAPQAVISSVNETSLMEWTPPRDSGGREDLVYNIICKSCGAGAGASCSRC 392  
362 GDNVOYAPROLGTEPRYISDLAHTQYFETIOAVNGVDSPEFOPASVNTTQAA 421  
393 DDNVEFPRQLGISEPRVHTSHLAHTRTYFEVQAVNGVSGSKPLPRRAAVNTTQAA 452  
422 PSAVSIHNOVSRTVDSITLMSQPDQNGVILDELOYEKEKELSEYNATAIKSPNTV-- 479  
453 PSEVPTLRLHSSSGSILTSMAPERPENGILDEYEMKYEK--SEGIASTVTSQMSVOL 510  
480 TGKACAIVFOYRATVAGYGRYSKMTFQMTTE--AEYOTSTOEKPLIIGSSAAGLVF 538  
511 DGLRPDARYVOYRATVAGYGRYSKMTFQMTTE--AEYOTSTOEKPLIIGSSAAGLVF 570  
539 LIAVVAIYVNCNRGFERADSEYTDKLOHYTSGHITPGKITYIDPPTYEDPNEAVREFAK 598  
571 VAANVAIYVNCNRGFERADSEYTDKLOHYTSGHITPGKITYIDPPTYEDPNEAVREFAK 626  
599 EIDISCVKIEOYIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLEASIM 658  
627 EIDVSCVKIEEYIGAGEFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDFLEASIM 686  
659 GOFDHPNVIHLEGVYTKSTPVMITTEFEMNGSLDSTLRNDQGFYIOLVGMRLGI 718  
687 GOFDHPNVIHLEGVYTKSTPVMITTEFEMNGSLDSTLRNDQGFYIOLVGMRLGI 746

[illegible]

Dh	157	VDTIAPDESFSLDAG----	RVNTYRREFGPLSKAGFLTAQDQACMSLISVAATFKKC	21.2
Qy	184	PHIIONGALFOETLGSABSTLSVAARSGCIANAEEVDVPIKLYCNGDGEMLVPIGRMCK	24.3	
Dh	213	ASTTAGFALFPELTLLGABETSLVIAFGPICINAAVEVSLPLKLYCNGDGEWVPVACTCA	27.7	
Qy	244	AGFEAVENGTVCYRGCPGSGFKNQDDEACTHCPIINSRTTSGAIVNCYCRNGYVADI.DPL	30.8	
Dh	273	TGHEPAAKESQCRPCRPSPSYKAKQGEQCECLCPSPRSRTTSPMAISICTCHNNFTYADSDSA	33.2	
Qy	304	DMPCTTISAPAOVAIVSSVNETSLMLEWT.PPRDSSGREDLVYNIITCKSC--GSGNACTRC	36.1	
Dh	333	DSACTTVPSPRGVINSNNETSLLEWSEBPDLGVRODLLVNYCKCHAGCASASCRC	39.2	
Qy	362	GNNVQYAPRQJLGT.PRIYIDOLAHQTYPEIDQAVNGVTDOSPFSPOFASVNTTMOA	42.1	
Dh	393	DNWVEFYERQJLSRPRYHTSHLARTTYTEVOAVNMGSKSP.LPRIAIVANTTMOA	45.2	
Qy	422	PSAVS.IHMOVSRTYDSTLSNSQDPQNGVILDYELQYEXELSEYNATAIKSPNTV--	47.9	
Dh	453	PSEVPTLRLHSSGSSLTSLNAPBERPNCVILDEMYEFEX--SEGIASTVTSQMSNVQL	51.0	
Qy	480	TGLKAGIYEVQVRRARYATAGYGRYSKMKY.POTIME--AEQTSIOEKPLIITGSAGLVF	53.8	
Dh	511	DGLRDAYVYVQVARYATAGY.GQY.SRAPEFTTSEKRSQAQLOEQJLPLVGSATGVLV	57.0	
Qy	539	LIAVVYVAIVCNRGFEADSEYTDKLOHYTSGHITFGMK.IYIDPTYEDDNEAVREFAK	59.8	
Dh	571	VAVVVYVAIVCLRKORHOSDEYTEKLOQY---IAGMKVYIDPTYEDDNEAVREFAK	62.6	
Qy	599	EIDISCYVIEBOVIGAGEGECVSHLKLPGKREIFVAIKTLGSPYRKORDFLSEASIM	65.8	
Dh	627	EIDVSCVAKIEEYVIGAGEGECVCRRLQOPGKREYFAVAKTLGKYGTERKORRDLSEASIM	66.6	
Qy	659	GOFDHPNVIHLEGVYNTSTPYMITTEFMENGSJDSFLRONDGQFTYVQIOLGMLRGIAAGM	71.8	
Dh	687	GOFDHPNIIIEGCVYNTSKRPYMITTEFMENCALDSFLRLNDGQFTYVQIOLGMLRGIAAGM	74.6	
Qy	719	KYLDMMNVVHEDLAAARNLTVNSNLVCVSPFGS.RLEDDTDSPTYSALGCGFPRI.RWTA	77.8	
Dh	747	KYLSBMNVVHEDLAAARNLTVNSNLVCVSPDGS.RLEDDTDSPTYSALGCGFPRI.RWTA	80.6	
Qy	779	PEALQYRKFTSASDWSYGYIWMVEVMSYGERPYVDMTNOVINAIEODYRL.PPMQCPSA	83.8	
Dh	807	PEALAYRKFTSASDWSYGYIWMVEVMSYGERPYVDMSNQOVINAVBQDYRL.PPMQCPSA	86.6	
Qy	839	LHOJLMOQMOCDRHHRK.FQGIYVTLTDKMLRNPSLKLAAAP.LSSGJNLPLLDRTIDYTS	89.8	
Dh	867	LHOJLMOQMOCDRHHRK.RKFSOIYVTLTDK.LLRNAA.SLKVLA.SAOSGMSQPLDRTYVDTYTT	92.6	
Qy	899	FNIVDEMLEIAIKMQGYESEFANAGFTSFVDVASSOMMEDILRYGVTTLAGHQK.LINSIQYM	95.8	
Dh	927	FTYVGMIDMLDAIKMGRYKESFESVAGFASFDLVQAQMTEDLLRGITVTLAGHQK.LTSSIQDM	98.6	
Qy	959	RAQNNQIQSEVY 970		
Dh	987	RLQNNQIQTLPVQV 998		

```

RESULT 14
PCT-US95-04681-20
: Sequence 20, Application PC/TUS9504681
: GENERAL INFORMATION:
: APPLICANT: Fox, Gary M.
: TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Amgen Patent Operations/RBW
: STREET: 1840 Dehavenland Drive
: CITY: Thousand Oaks
: STATE: California

```



```

Query Match      70.0%: Score 3595.5; DB 2; Length 970;
Best Local Similarity 70.0%; Pred. No. 1,6e-266;
Matches 671; Conservative 115; Mismatched 161; Indels 11; Gaps 4.

OY 16 TAEIGMNVHPSPGMEVSYGDENMMNTIRTYQOVNVESSQNNMLRTKRIIRRCANHIVE 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 TSELAAMTHETGEEVSYGDAMOPIRTYQOVYREAOQOOLRKRFINRQDVQAYIVE 80
OY 76 MKFEVRCCSSIPSPGCKETENLYYEADFSAITTFPMEMENPVKYDTIADESFO 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 81 LKFTVRCRCKSIPIKPGCKETENLFYESTSDSASNSPMEENPIKXDTIAPDESFSK 140
OY 136 VDLGVRMYKINTEVRSFGVSRSGFYLAOFDYGCSASLJAVRFRYKCPRIIONGAIPE 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 LESG---RVNTKYRSFGPLSKNGFYLAODIGACMSLILVAFYKCKSNTIAGFAIPE 196
OY 196 TLISGASTSLVAARGSCINAAEVDYPIILYKCGDEMLVPIGRCKCKAGFEAVENGTVG 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 TLTGAEPTSLVLPCTGICPOAAEVSPILYKCGDEEMVPPGACTCAGAYEPAPKADQC 256
OY 256 RCGPSTFRANOGDEACTHCPIINSRTSGATNCVGRNGYVRADDPIDMPTTIPSAPO 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 QACGPSTFRSKQEGEPCPCPPSRSTTAAATVCIORSGFFPADPADPSACTSVSAPR 316
OY 316 AVTSVNNETSLMEEMTPPDSDGREDLYNIITCKSGSGRGACTRCGDNVOYAPRQLLT 375
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 317 SVTSVNNETSPLEWSEPDAGGRDOLLVNIICKCSVERILCSRDDNVEFVRPQLLT 376
OY 376 EPRYITSDLAITYFFELIOAVNGVLYDPSFOPASVITITNOAPASVSIIMHOVSTV 435
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 377 ERRITYSKVMAHQYTFEIOAVNGVSIKSPYPRHPSAVNITITNOAVLSAVPMLHSTG 436
OY 436 DSTLTSMSPPDPNGVILDYELQYIEKE--LSTYNATAIKSPNTV--TGLAGAIYVRQV 492
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 437 NSMTLSMTPEPENGILIDYEIKYSEKQGGGINTYTSOKNSVRDLGALKANARYMVQ 496
OY 493 RARTVAGYGRYSKMVFQTMTEAEYQTSIOEKLPTIISAAAGLFLTAVVVIATVCCR 552
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 497 RARTVAGYGRYSLTPEFQTAEDGSTKTFQGLPIVGSATRAGLLFVIVYITAIYCRK 556
OY 553 GERPADSEYTKDLOHYTSGHITPGKIKYIDPPTYEDPNAVREPAKETIDISCVKIEOYIG 612
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 557 QANSTDPETTELQOY---VTPGKAYVIDPPTYEDPNAVREPAKETIDISCVKIEEYIG 612
OY 613 AGEFEVCSGLHLRPGKREIFAVALTKLSGYTEKORRPFLEASIMQFDPHPIHIEGV 672
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 613 AGEFEVCRGRKLTPGKREIFAVALTKLVGYTERORRPFLEASIMQFDPHPIHIEGV 672
OY 673 VRSPPVMIITFEFMNGSLDSFLRNDQOFVIOUYGLRILAIAGMKTYLADMTVVRHDLA 732
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 673 VTKSRPVIATVEEMNCALDSFLRLKNDQOFVIOUYGLRILAIAGMKTYLSEMNVAHDLA 732
OY 733 ARNILLVNSNLVCKVSDFGLSRFLEDDTSDPTYTALSGLKFPRIINTARAEALORYKFTSASD 792
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 733 ARNILLVNSNLVCKVSDFGLSRFLEDDPADPYTSSLGKIPRIINTARAEALVAKRFTSASD 792
OY 793 VWSYGVIVMWEVMSGERPYMTNODVYNALEOYRILPRPHDCSALHQLMDQCKDRN 852
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 793 VWSYGVIVMWEVMSGERPYMTNODVYNALEOYRILPRPHDCSALHQLMDQCKDRN 852
OY 853 HRPKFGQIVNTLDKMIIRNPNSLKAAPLSSGINPLDRTIPDTSFNPTDEWLAIKMG 912
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 853 LRPKFAQIVNTLDKILIRMAASLKVIASQVSGVPLADRTIVPDYTTFTYGDMLDAIKMG 912
OY 913 QYKSEFAVAGCTSPDYVSOMMEDILVGVYGLGHOKKILNSTQVMAQONQIOSEV 970
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 913 RYKENTVHHGASDVLVAQMTAEIDLIGVYGLGHOKKILNSTQVMAQONQIOLPVOY 970

```

Search completed: July 24, 2001, 16:29:09  
Job time: 345 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2001, 16:21:49 ; Search time 24.02 Seconds

(without alignments)  
2448.179 Million cell updates/sec

Title: US-09-378-759-11

Sequence: 1 LLAIVETLMDSSTATAELG.....ILNSIQVRAQMNIQSVEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: /SIDSB8/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSB8/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSB8/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSB8/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDSB8/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDSB8/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDSB8/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDSB8/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDSB8/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDSB8/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDSB8/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDSB8/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDSB8/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDSB8/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDSB8/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDSB8/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDSB8/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDSB8/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDSB8/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDSB8/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDSB8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDSB8/gcgdata/geneseq/geneseq/AA2001.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5116	100.0	970	AA85089	EPH-like receptor
2	5092	99.5	1055	AA819591	Human CASB616
3	5082.5	99.3	987	AA819590	Human CASB616
4	5082	99.3	994	AAW26366	Human NUK tyrosine
5	4950.8	99.3	994	AA887018	Receptor tyrosine
6	4934.5	98.5	1011	AA875712	EPH-related PTK Ce
7	4906.5	98.5	1011	AA875709	EPH-related PTK Ce
8	3906.5	72.3	984	AA844513	elk. Rattus rattu
9	3698.5	72.3	951	AA875704	EPH-related PTK Ce
10	3656	71.5	973	AA875708	EPH-related PTK Ce
11	3649.5	71.3	988	AA875710	EPH-related PTK Ce

12	3622.5	70.8	990	AA851899	Human embryonal K1
13	3590.5	70.2	993	AA875843	Protein p140 CDNA
14	3590.5	70.2	993	AA875844	Protein p140 CDNA
15	3326.5	65.0	973	AA875707	EPH-related PTK Ce
16	3031	59.2	986	AA885091	EPH-like receptor
17	3031	59.2	991	AA885090	EPH-like receptor
18	3024	59.1	986	AA885936	Protein tyrosine-k
19	3016	59.0	998	AA885092	EPH-like receptor
20	3001	58.7	998	AA885092	EPH-like receptor
21	2918.5	57.0	983	AA808655	Mouse developmenta
22	2917.5	57.0	983	AA808655	Amino acid sequenc
23	2910	56.9	983	AA875711	A human EPHA3 HLA
24	2907	56.8	1005	AA883147	EPH-related PTK Ce
25	2889.5	56.5	983	AA831466	Rat receptor tyros
26	2827.5	55.3	987	AA889263	Human non-differen
27	2827.5	55.3	987	AA889263	Protein tyrosine-k
28	2827.5	55.3	987	AA806335	Full length recept
29	2827.5	55.3	987	AA806335	Receptor type tyro
30	2825.5	55.2	987	AA894652	Receptor type tyro
31	2816.5	55.1	972	AA876468	Maternal non-differ
32	2816.5	55.1	972	AA876468	Full-length recept
33	2780.5	54.3	1293	AA841896	PTK gene HPRK5 pro
34	2714.5	53.1	849	AA875706	EPH-related PTK Ce
35	2611.5	51.0	928	AA875706	Rat REK7 eph-relat
36	2600	50.8	948	AA883148	Rat receptor tyros
37	2442	47.7	877	AA871628	Mouse BSK receptor
38	2439	47.7	1006	AA870525	Human thymus recep
39	2439	47.7	1021	AA870526	Human thymus recep
40	2438	47.7	1006	AA872256	Human thymus recep
41	2256	44.1	722	AA875705	EPH-related PTK Ce
42	2238	43.7	744	AA875713	EPH-related PTK Ce
43	2167	42.4	710	AA875714	EPH-related PTK Ce
44	1951.5	38.1	856	AA827656	Human protein PRO3
45	1871.5	36.6	977	AA819258	Embryonic stem cel

#### ALIGNMENTS

```

RESULT 1
AA85089
AA85089 standard; Protein: 970 AA.
AC
AA85089;
DE
16-APR-1996 (first entry)
EPH-like receptor protein tyrosine kinase HEK5.
KW
human eph-like kinase; therapy; diagnosis; vector; antibody.
OS
Homo sapiens.
PN
WO9528484-A1.
PD
26-OCT-1995.
PF
14-APR-1995; 95WO-US04681.
PR
15-APR-1994; 94US-0229509.
PA
(AMGE-) AMGEN INC.
PI
Fox GM, Jing S, Welcher AA;
XX
WPI: 1995-373799/48.
XX
N-PSDB: AAT02946.
XX
New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -
XX
and related vectors, host cells, proteins, antibodies etc., used
XX
diagnostically and therapeutically to modulate receptor activation
XX
or prodn.
PT

```





Query Match 99.58; Score 5092; DB 21; Length 1055;  
Best Local Similarity 99.68; Pred. No. 0;  
Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

1 LLAAVEETLMSTTATAEIGMNVHPSPGWEVSGYDENMNTIRTYOVNVPESSONMRLR 60  
15 llaaveetlmstataeiglmvhpssgweevsgydenmnlrtlyqvcnvfessqnmwlr 74  
61 TKFIRRGAGRHIHVMKFSVDCSSIPVPCSKETENLYYEADPDSATKPFPMNBNP 120  
75 tkfirtirgagrhlhvmkfsvdcsslpsvpscketfnlyyeaddfsactkfpnmwmp 134  
121 WVKVDTIADSFQVLDGGMKINTEVRSFGVSRSGEFLAFQDYGCCNSLIARVRY 180  
135 wkvvdtiaadefsqvldggrvmkintevrsfgvrsrgfyldfydgycnsliarvrfy 194  
181 RKCPRIIONGAIFQETLSGASTSLVARGSCIANAEVDVPIKXNCGDEMKVPIGRG 240  
195 rkcpriiongaifqetlsgaestslvaargscianaevdvplklycngdgewlvpiigr 254  
241 MCKAGFEAVENGTVCRGCPSGTFRANOGDEACTHCPINSRTTSGATNCVCNRYRADL 300  
255 mckagfeavengtvcrpgsgtfrkangdeacthcnprtsgatncvcrnryradl 314  
301 DPLMPCTTISARQAVIYSSNETSLMEWTPPDSCGREDLVYNIICKSCSGRGACTR 360  
315 dplmpcttisarpqavissnetslmewtppdscgredlvyniickscsgrgactr 374  
361 CGDNVQYAPRQLGLEPRITVSDLAHTQYTFEIOAVNGVYDOSPFSPFQSVNITNOA 420  
375 cgdnvqyaprlglepritysdlahtqytfelqavngvldgspfpqslasviltnga 434  
421 APSAVSIHMOVSRVTSITLSWSQPDQNGVILDYELQYKEKSEYNATAIKSPNTVT 480  
435 apsavsihmovsrvtstlswsqpdqngvildyelyksekseynataikspntvt 494  
481 - -GLKAGAIYFOYRARTVAGYGRYSGKMYFQYTAETAEYQTSIOEKPLIIGSSAAGLV 538  
495 vqgikagailvyfgrartvagygrysgkmyfqteteeaytsiqekpliliggsaaglv 554  
539 LIAVVVAIYCNRRGFERADSEYTDKLOHTSGHITPGMKIYIDPPYEDPNEAVREFAK 598  
555 liavvvaiycnrrgferadseytdklohtsghtpgmklyidppfyedpneavrefak 614  
599 EIDISCVKIQVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORRDFLSEASIM 658  
615 eidiscvkiqvigagefgevcsghlkgpreifvaiktlksgytekorrdflesasim 674  
659 GOFHPRVHILEGVYVTKSTPVMITTEFMENGSLDSFLRONDGQFTVQLVGMRLGIAGM 718  
675 gofhprvhilegvvtskstpvmittetfmgslsdlrondgqftvqlvgmrlrglaagm 734  
719 KYLADMYVHRDLAARNILVNSNLVCVDFGSLRFLDSTDPSTYSALGKFPRTWTA 778  
735 kyladmyvhrdlaarnilvnsnlvcvdfgslrfldestdpstysalrgkfpirtwa 794  
779 PEALQYKFTSASDVSYGIVMEVWSYGERPYWDMTNDQVINAIEQDYRLPPMDCPSA 838  
795 pealqykftsaadvsygivmewwsygerpywdmtndqvinaieqdyrlppmdcpse 854  
839 LHLMLDCKMOKDRNHRKFGQIYNTLDKMTIRNNSLKAAAPLSSGILNPLLDRTIDYTS 898  
855 lhlmldckmokrnhhrkfgqiynltldkmtirnnslkaaplssgilnplldrtidyts 914  
899 FNTVDEMLEAIKMGQYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHOKITLNSIQVM 958  
915 fntvdeMLEAIKMGYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHOKITLNSIQVM 974  
959 RAQMNOIQSYVE 969  
975 raqmnoiqsyve 985

RESULT 3  
AAB19590  
ID AAB19590 standard; Protein: 987 AA.

XX AAB19590;

DT 22-JAN-2001 (first entry)

XX Human CASB616.

XX CASB616; EPHB2; ERK; EPH3; EPH3; DRT; HEK5; EPHB2v;  
KW receptor protein tyrosine kinase; human; antigen; colon cancer;  
KM ovary cancer; tumour; autoimmune disease; vaccine; therapy;  
KM diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT MISC-difference 568..569

FT /note="an additional Arg residue decodes from the  
FT CASB616 nucleotide sequence given in the  
FT specification (see AAB8548), but is not  
FT given in the CASB616 amino acid sequence in  
FT the specification"

FT MISC-difference 956

FT /note="encoded by GTT"

PN W0200053216-A2.

XX 14-SEP-2000.

PD 28-FEB-2000; 2000MO-EP01587.

XX 05-MAR-1999; 99GB-0005124.

PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.

PI Vinals De Bassols YC;

DR WPI: 2000-587384/55.

DR N-PSDB; AAB8548.

PT Vaccine composition for treating ovarian and colon cancer, comprises  
PT CASB616 polypeptides, polynucleotides or antigen presenting cells  
PT expressing the polypeptides  
PS Claim 1; Page 41; 57pp; English.

XX The present sequence is that of human CASB616, a member of the EPH  
CC and EPH-related family of receptor protein tyrosine kinases.  
CC CASB616 is also known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and  
CC EPHB2v. CASB616 polypeptides and polynucleotides are important  
CC immunogens for specific prophylactic or therapeutic immunization  
CC against tumours, especially colon cancer (claimed) and ovarian  
CC cancer. They are specifically expressed or highly over-expressed  
CC in tumours compared to normal cells and can thus be targeted by  
CC antigen-specific immune mechanisms leading to destruction of the  
CC tumour cells. They can also be used to diagnose the occurrence of  
CC tumour cells. Their inappropriate expression can also cause an  
CC induction of autoimmune responses, which can be corrected through  
CC vaccination using the CASB616 polypeptides or polynucleotides.  
XX Sequence 987 AA.

Query Match 99.38; Score 5082.5; DB 21; Length 987;  
Best Local Similarity 99.48; Pred. No. 0;  
Matches 967; Conservative 2; Mismatches 1; Indels 3; Gaps 2;

1 LLAAVEETLMSTTATAEIGMNVHPSPGWEVSGYDENMNTIRTYOVNVPESSONMRLR 60  
15 llaaveetlmstataeiglmvhpssgweevsgydenmnlrtlyqvcnvfessqnmwlr 74

```

QY 61 TFEIRRRGARHRIHVENKESFVRDCSSIPSVGCKETFNLYYEADFDASVTKTFPMNMENP 120
  |||
  |||
  |||
Db 75 kffirrrghrhlhvemkfvdrdcssipsvgsketfnlyyeadfdsatkflpmnem 134
  |||
  |||
  |||
QY 121 WKVVDTIADSEFSQYDLGGRWKINTFVRSRGPVSRSGFYLAFOYGGCMSLIARVRY 180
  |||
  |||
  |||
Db 135 wkvvdtaadesfsqydlggrywklntfvrsvrsgfylafoqyggcmsliarvry 194
  |||
  |||
  |||
QY 181 RKCPRIIONGAIFOETLSGAESTSLVAANGSCIANAEVDVPIKICNDGEMLVPIGRNC 240
  |||
  |||
  |||
Db 195 rkcpriiongaifgetlsgaestsivaangscianaeevdvpiklycngdgemlvpiygrc 254
  |||
  |||
  |||
QY 241 MCKAGFEAVENGTVCRGCPSPGTFKANQGDACHCPINRRTTSEGATNCVCNRNGYRABL 300
  |||
  |||
  |||
Db 255 mckagfeavengtvcrpcspgtfkanqgdeachcpinsrttsegatncvcnryyradl 314
  |||
  |||
  |||
QY 301 DPLDMCCTTIPSPAPAVISVNETSLMELMTPPRDGSREDLVYNTICKSCSGSGACATR 360
  |||
  |||
  |||
Db 315 dpldmccclipsapavisvnetslmlewtpprdsgredlvynlickscsgsgractr 374
  |||
  |||
  |||
QY 361 CGDNVOYAPROLOLTPPRIYISDLAHTQYTEPIQAVNGVTDOSPSPQFASVNTTNOA 420
  |||
  |||
  |||
Db 375 cgdnvoyaprqjlltprilyisdlahqtlyteiqavngvtdospqfasvntltnga 434
  |||
  |||
  |||
QY 421 APSAVSIMHOVSRVSTILSMQDPQNGVILDYELQYREKLSRYNATIKSPNTVT 480
  |||
  |||
  |||
Db 435 apsavsimhovsrvtstlsmwqdpqngvildyelyrekelesynatalkspntvt 494
  |||
  |||
  |||
QY 481 --GLKGAIVFQVARTVAGRYSGKMFQMTAEQTSIOEKLPLITIGSSAGLVF 538
  |||
  |||
  |||
Db 495 vglkagalyvfvartvagyrysgkmyfqmtaeqtsioekpliliggsaaglvf 554
  |||
  |||
  |||
QY 539 LAVVAVIAVCN--RKGPERADSEYTDKLOHTYSGHITPGMKIYIDPPTYEDNEAVEA 597
  |||
  |||
  |||
Db 555 lavvavaivcnrrrgeradseytdklqhtysghmtpgmkiiydpfityedneavea 614
  |||
  |||
  |||
QY 598 KEIDISCVKTEQYIGAGEGECVSGHUKLPGRKEIFVAKITLKSGETEKKORRFLSEAS 657
  |||
  |||
  |||
Db 615 keidiscvkteqyigagegecvsgnhklpgrkeltvaiklksygekrflseasl 674
  |||
  |||
  |||
QY 658 MGOFDHPNVITHLEGVVTKSTPVMIIIEFMEGSLDSFLRONDOQFVYDQVLMRLGIAAG 717
  |||
  |||
  |||
Db 675 mgofdhpnvithlegvvtkstpvmlitefmeagsldelfrqndqgfcvqivgmrlgiaag 724
  |||
  |||
  |||
QY 718 MKTLADMTYHRLAARNILVNSNLVCKVSDGSLRPLEDTSDPYTSLAGKRPFRWT 777
  |||
  |||
  |||
Db 735 mkyladmnyhrdlaarnilvnsnlvckvsdglsrpledtsdpytsalagkrlpfrwt 794
  |||
  |||
  |||
QY 778 APEAIQYRKFTSADWSYGIWMEWMSYGERPYMDTNDVINAIEQDVRRLPMDPCPS 837
  |||
  |||
  |||
Db 795 apaiaiqyrtksadwsygiwmeewmsygerpywdmtndvinalieqdyrlpmdpcps 854
  |||
  |||
  |||
QY 838 ALHQLMLDCQKQNRNHRKFGQIVNTLDKMIIRPNLSLKAMAPLSSGINTPLDRTIPTYT 897
  |||
  |||
  |||
Db 855 alhqmldcqkqnrnhrkfgqivntldkmirpnlskamaplassgintpldrtlptyt 914
  |||
  |||
  |||
QY 898 SFTNVDBMLEAIKMGQYKESFANAGTSPVVSQMMEDILRQVTLRVLGQKILINSIOY 957
  |||
  |||
  |||
Db 915 sftnvdbmleaikmqykesfanagtspvvsqmmmedilrqvltlragqkilknsioy 974
  |||
  |||
  |||
QY 958 MRAOMNIOSEVY 970
  |||
  |||
  |||
Db 975 mraqmqiqsevey 987
  |||
  |||
  |||

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RESULT 4  
 AAM26366  
 ID AAM26366 standard; Protein; 994 AA.  
 XX  
 AC AAM26366;  
 XX  
 DT 02-DEC-1997 (first entry)

```

XX DE Mouse Nuk tyrosine kinase.
XX Nuk tyrosine kinase; Eph receptor tyrosine kinase;
XX signal transduction; axonogenesis; neurodegenerative disease;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX multiple sclerosis; amyotrophic lateral sclerosis;
XX Kernerick's disease; nerve damage; trauma; ischemia; stroke.
XX
XX OS Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /label= Sig-peptide
XX Protein 27..994
XX /label= Mat-protein
XX Domain 27..548
XX /label= Extracellular_domain
XX Region 330..420
XX /label= FNIII
XX /note= "fibronectin type III repeat"
XX Region 444..534
XX /label= FNIII
XX /note= "fibronectin type III repeat"
XX Domain 549..574
XX /label= Transmembrane_domain
XX Domain 575..994
XX /label= Cytoplasmic_domain
XX Region 623..888
XX /label= Tyrosine-kinase_region
XX
XX PN W09714966-A1.
XX
XX PD 24-APR-1997.
XX
XX PF 10-OCT-1996; 96WO-CA00679.
XX
XX PR 13-OCT-1995; 95US-0005518.
XX
XX PA (MOON ) MOUNT SINAI HOSPITAL CORP.
XX
XX PI Henkemeyer M, Pawson A;
XX WPI: 1997-245245/22.
XX DR N-PSDB; AAT84528.
XX
XX PT Activation of ligand regulatory pathways by Eph subfamily receptor
XX tyrosine kinases - for stimulating or inhibiting axonogenesis,
XX useful for treatment of e.g. neurodegenerative diseases such as
XX Alzheimer's or Parkinson's diseases
XX
XX PS Disclosure: Fig 3; 5pp; English.
XX
XX CC Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine
XX kinase that is essential for formation of the medial tract of the
XX anterior commissure of the brain, and which appears to play a
XX role in the formation of the habenular interpeduncle tract. Its
XX amino acid sequence was deduced from cDNA clones (see AAT84528)
XX isolated from an embryo cDNA library. The extracellular domain
XX of Nuk was shown to be sufficient for formation of the medial
XX tract. Eph subfamily receptor tyrosine kinases (e.g. the Nuk
XX extracellular domain) can be used in claimed methods to: activate
XX a ligand regulatory pathway in a cell; identify substances able to
XX bind a ligand for an Eph subfamily receptor tyrosine kinase; and
XX to affect neuronal development or regeneration, especially the
XX stimulation or inhibition of axonogenesis, in a mammal. Activation
XX of the ligand regulatory pathway results in downstream activation
XX of a series of regulatory pathways in cells that control gene
XX expression, cell division, cytoskeletal architecture, cell
XX metabolism, cell migration and cell-cell interactions. Substances
XX which activate the ligand regulatory pathway may be used for
XX stimulating or inhibiting neuronal development regeneration and
XX axonal migration associated with neurodegenerative disease e.g.
XX

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CC Alzheimer's, Parkinson's or Huntington's diseases, multiple  
 CC scleriosis, amyotrophic lateral sclerosis, deficiency diseases such  
 CC as Wernicke's disease, peripheral nerve damage, trauma and  
 CC ischemia resulting from stroke.  
 XX

Sequence 994 AA:

Query Match 99.3%; Score 5082; DB 10; Length 994;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

```

OY 1 LLAAEETLMOSTTAAELGMMVHPSPGMEYSGYDEKMNNTIRTYQVCNVESSONMLR 60
DB 23 LLAaveelmdstcataelgmmvhpssgweevsgydenmnlrltygvcnvfessqnnmlr 82
OY 61 TFFIRRGARHRIHVMKFSVRDCSSIPSPGCKETFLYYEYEDFSDATPFPMNMENP 120
DB 83 tkfrrrgahrhvmkfsvrdcssipspgcketflnyyeadfdlatkctfpmnenp 142
OY 121 WKKVTITAADESFQVLDGGRVMTNTEVRSFGVRSGLAFADYDGGCSLJAVRVEY 180
DB 143 wkvvtitaaadesfsgvldggrvmtntevrsfgvrsngfyldqdygscsljavrvfy 202
OY 181 RCPRIIONGAIFOETLSGAESTSLVARGSCIANAEVNDPIKLYCNGDGEMLVPIGRG 240
DB 203 rkcpriiongaifgetlsgaeestslvaarsgclanaeevndpiklycngdewlvpiigr 262
OY 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPIKSRTPSGATNCVCRNGYRADL 300
DB 263 mckagfeavengtcvrcgpgsgtfkangdeacthcinrtsegaencvcrngyradl 322
OY 301 DPLMPCTTISARQAVIASSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
DB 323 dplmpcttisarpqaviasvnetslmewtpprdsgrredlvnyllicksgsgrgactr 382
OY 361 CGDNQVAPROLGLTEPRITYSDDLTAHTOYTFEIOAVNGVTDOSPSPROFASVNTTNOA 420
DB 383 cgdnvaprolgltepritysdldtahtoytfeioavngvtdospspropfasvnttnoa 442
OY 421 APSAVSTMHOVSRTVDSITLWSQPDOPNGVILDYELQYEEKELSEYNAAVAKISPTWTVT 480
DB 443 apsavstmhovsrtvdsitlwsqpdopngvildyelyekelseyenaaavakispwtvt 502
OY 481 --GKAGATVFOYBARTVAGYGRYSGKMYFQMTAEYOTSIOEKPLITIGSSAGLVF 538
DB 503 vggikagatvfoybartvagygrysgkmyfqtmtaeysioekplilvgssaglvf 562
OY 539 LIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHTPGMKIYIDPFYEDPNCAVREFAK 598
DB 563 liavvviavcnrrgfesradsedytdklohtsghtpgmkityidpfyedpncavreftak 622
OY 599 EIDISCKIKIOVIGAGFGEGVCSGHLKPGKREIFAIAIKTLKSGYTEKORDELSEASIM 658
DB 623 eidiscvikiovigagfgvcsghlpgkreifaiaiktlksgytekordeleseasim 682
OY 659 GQEDHPNVIHLEGVYFSTPVMITTEFMENGSLSDFLRQNDGPFYIOLVGMIRGIAAGM 718
DB 683 gqedhpnvihlegvyfstpvmittetfmengsldsfllrqndgpfyiolvgmirgiaagm 742
OY 719 KYLADNMVYVRDLAARNILVNSLVCKVSDPGLSRFLIEDTSDPTYSALGCFPIRMTA 778
DB 743 kyladnmvyvrldlaarnilvnsllvckvsdpglsrfliedtspdytsalpgkpirmta 802
OY 779 PEAIORYKFTSASDVWSYGVIMVEVMSYGERPYMDTNDVINAIRQDYRLPEPMDCPSA 838
DB 803 peaiorykftsasdvwsygvimvevmsygerpymdtndvinaireqdyrlppepmcpsa 862
OY 839 LHOGLMDQWQDRNHRPKFGQIVNTLDKMI RNPNSLKAAAPLSSGGINLRLDRTIPDYTS 898
DB 863 lhgldmqwqdrnhprkfgqivntldkmlrnpnslikaaaplssgginrlldrtipdyts 922
OY 899 FNVVDMLKAIKMGYKESFANAGFTSFVDSOMMMEDILRAGVTTLACHQKILINSIQVM 958

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DB 923 fntvdeleakngqkytesfanaqfcsfvvssqmmmedilrvgtclagqkklinsiqvm 982
OY 959 RAQMQIOQSEV 970
DB 983 raqmqiqsvev 994

```

## RESULT 5

AA87018  
 ID AA87018 standard; Protein; 994 AA.

AA87018:

19-MAR-1996 (first entry)

Receptor tyrosine kinase (neural kinase).

Receptor tyrosine kinase; neural kinase; Nuk; axon;  
 axonogenesis; nerve disorder.

Mus musculus.

Key  
 Peptide  
 Location/Qualifiers

1..26  
 /label= Sig-peptide

27..548  
 /label= Extracellular-region

/note= "The extracellular region (amino acids  
 27-548) includes an N-terminal Ig-like  
 domain and an Ig-like Nuk repeat"

330..420  
 /label= FNIII

/note= "fibronectin type III repeat"

444..534  
 /label= FNIII

/note= "fibronectin type III repeat"

549..574  
 /label= Transmembrane-region

575..994  
 /label= Cytoplasmic-region

623..707  
 /label= Tyrosine-kinase\_catalytic\_domain

MO9530326-A1.

09-NOV-1995.

28-APR-1995; 95WO-CA00254.

29-APR-1994; 94US-0235407.

(MOUNT ) MOUNT SINAI HOSPITAL CORP.

Henkemeyer M, Letwin K, Pawson A;

WPI; 1995-393299/50.

N-PSDB; AAT07308.

DNA encoding neural receptor tyrosine kinase - useful in gene  
 therapy of nerve disorders, and for diagnosis and identification of  
 therapeutic agents

Claim 1; Page 70-74; 103pp; English.

A novel receptor tyrosine kinase (AA87018), designated neural kinase  
 (Nuk) (AA87018), is encoded by cDNA (AAT07308) obtd. from a mouse  
 embryo library. Nuk is expressed in migrating axons and is  
 involved in cell-cell interactions and axonogenesis in development  
 of the nervous system. Nuk or its fragments (pref. amino acids  
 26-548 or 601-994) are used to identify (ant)agonists of the  
 (activated) receptor tyrosine kinase as a means of treating nerve  
 disorders and damage, or to raise antibodies used to monitor axon

CC migration and nerve cell interactions.

XX Sequence 994 AA:

Query Match 99.3%; Score 5078; DB 16; Length 994;  
Best Local Similarity 99.1%; Pred. No. 0;  
Matches 963; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

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QY 1 LLAAVEETLMDSTTAAELGMMVHPPSGMEVEVSGYDENMNTIRTYOVCAVPESSONMLR 60
    |||
DB 23 llaaveelmdstlaelgmmvhpssgweevsgydenmnlrtlyqvcnfessqnmwlr 82
    |||

QY 61 TKFIRRGARHRIHVEKFSVRDCSSIPSPGSKETFNLYYEADPDSATKTFPMNMENP 120
    |||
DB 83 tkfrrrgarhrihvekfsvrddcssipspgsketfnlyyyeadtdlatktfpmnmep 142
    |||

QY 121 WVKVDTIAADESFQYDLGRVVKINTEVRSFGVRSGFYLAFOYGGCMLIAVRVY 180
    |||
DB 143 wkvdtlaadesfsqydlgrvvnkintevrsfgvrsngfyiafdyggcmliaavrly 202
    |||

QY 181 RKCPRRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDDGEMLVPIGRG 240
    |||
DB 203 rkcprriongaifoeetlsgaestsivaargscianaeevdvpkilycngdgewlvpiqrc 262
    |||

QY 241 MCRAGEFAVENGIVRCRCPSTFKANOGDEACTHCPINSRTTSEGAATNCVCRNGYTRADL 300
    |||
DB 263 mckagfeavengivrcrcpsgtfkangdeacthcpinsrttsegaatncvcrngyyradl 322
    |||

QY 301 DPLDMPTTIPSAPOAVISSVNETSLMLEWTPPRDSGGRDLVYNIICKSCSGRGACTR 360
    |||
DB 323 dpldmptclipsapqavissvnetslmewcprrdsgrdelvyniickscsgsgractr 382
    |||

QY 361 CGDNVQYAPRQGLGLEPRRIYISDLAHTQYTFELQAVNGVTDGSPSPQFASVNTITNQA 420
    |||
DB 383 cgdnvqyaprqglgleprriylsdlahatqytfelqavngvtdgspfpqfasvntitnqa 442
    |||

QY 421 APSAVSTIMHOYKRTVDSITITSMSPDOPNGVITIDELYEKEKELSEYNATATISPTVTW 480
    |||
DB 443 apsavstimbhoykrtvdsititlsmspdpngvildelyekekelseynatalksptvtw 502
    |||

QY 481 --GLKAGAIYFQYRARTVAGYGRYSKMYFQUTWEAEYTSIOEKLPLIIGSSAGLVF 538
    |||
DB 503 vglkagaiyfyqrartvavgrysgkmyfqtuweaeysioeklplilvgssaglvf 562
    |||

QY 539 LIAVVVIAIVCNRRGFERADSEYTDKLOHTSGHITTPGMKIYIDPFTEEDPNEAVREFAK 598
    |||
DB 563 liavvviaivcnrrgfereadseyltdklqhtsghttpgmkiyidpfteedpneavrefak 622
    |||

QY 599 EIDISCVKIEQVIGAGEGECVSGHLKPGKREIFVAIKTLKSGYTEKORRDFLEASIM 658
    |||
DB 623 eidiscvkieqvigagegecvsghlkpgkretfeivaiktlksgytekorrdflseasim 682
    |||

QY 659 GQFHPNVIHLEGVVTKSTPMIITTEFMENGSLDSFLQNDGQFTVITQLVGMGLGIAAG 718
    |||
DB 683 gqfhdprnvihlegvvtkstpmiitfefmengslsflrqndgqftvltqvlgmglgiaagm 742
    |||

QY 719 KYLADMTVHRDGLAARNTLVNSNLVCKVSDGSLRFLIEDTSDPPTYSALGGCKPIRMTA 778
    |||
DB 743 kyladmtyhrdglarntlvnsnlvckvsgdgsrlfledtspdptysalggckpirlmta 802
    |||

QY 779 PEALIOYRKFTSASDVWSYGIWMEVMSYGERPYMDMTNQDYNIAIEODYRLRPPMDPCSA 838
    |||
DB 803 pealioyrfkftsasdvwsygiwmevmsygerpymdmtntqdyniaieodgyrlppmdpcsa 862
    |||

QY 839 LHQMLDMQMDKDRNHRPFGQIVNTLDMKIRNPNLSKAMAPLSSGINSPLDRIPIPTYS 898
    |||
DB 863 lhqmldmqmdkdrnhrpfgqivntldmkirnpnlskamapllssginspldripipts 922
    |||

QY 899 FNTVDEMLIAIKMGQYKRSFANAGTSPDVYSOMMMEDILVGVTLACHOKKILINSIOVM 958
    |||
DB 923 fntvdeleakmgqykrsfanagtsfdvysommedilvgyvtaachgkklinsiovm 982
    |||

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QY 959 RAQMNQIOSVEY 970  
DB 983 raqmqdiqsvew 994

# RESULT 6

ID AAR75712 standard; Protein: 995 AA.

AA75712:

11-NOV-1995 (first entry)

Eph-related PTK Cdk5.

Cdk5; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;

prognosis.

Gallus sp.

W09515375-A.

08-JUN-1995.

07-SEP-1994; 94WO-US10140.

03-DEC-1993; 93US-C162809.

(LJOL-) LA JOLLA CANCER RES FOUND.

Pasquale EB, Sajjadi FG;

WPI: 1995-215256/28.

N-PSDB: AAQ90660.

Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing cancer.

Disclosure: Page 92-96; 129pp; English.

Probes derived from the Eph-related PTKs Cdk4 (AAQ90659) and Cdk5 (AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58, CC AAQ90661-62) from chicken embryo and embryonic brain libraries.

Sequence 995 AA:

Query Match 96.8%; Score 4950.5; DB 16; Length 995;  
Best Local Similarity 95.6%; Pred. No. 0;  
Matches 930; Conservative 28; Mismatches 12; Indels 3; Gaps 2;

```

QY 1 LLAAVEETLMDSTTAAELGMMVHPPSGMEVEVSGYDENMNTIRTYOVCAVPESSONMLR 60
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DB 23 llaaveelmdstlaelgmmvhpssgweevsgydenmnlrtlyqvcnfessqnmwlr 82
    |||

QY 61 TKFIRRGARHRIHVEKFSVRDCSSIPSPGSKETFNLYYEADPDSATKTFPMNMENP 120
    |||
DB 83 tkfrrrgarhrihvekfsvrddcssipspgsketfnlyyyeadtdlatktfpmnmep 142
    |||

QY 121 WVKVDTIAADESFQYDLGRVVKINTEVRSFGVRSGFYLAFOYGGCMLIAVRVY 180
    |||
DB 143 wkvdtlaadesfsqydlgrvvnkintevrsfgvrsngfyiafdyggcmliaavrly 202
    |||

QY 181 RKCPRRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDDGEMLVPIGRG 240
    |||
DB 203 rkcprriongaifoeetlsgaestsivaargscianaeevdvpkilycngdgewlvpiqrc 262
    |||

QY 241 MCRAGEFAVENGIVRCRCPSTFKANOGDEACTHCPINSRTTSEGAATNCVCRNGYTRADL 300
    |||
DB 263 mckagfeavengivrcrcpsgtfkangdeacthcpinsrttsegaatncvcrngyyradl 322
    |||

QY 301 DPLDMPTTIPSAPOAVISSVNETSLMLEWTPPRDSGGRDLVYNIICKSCSGRGACTR 360
    |||

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Db 323 dpydmpctllpsapqavlsenvetslmlewtpdrdsqaredlylnllckscsgsrgacr 382  
Qy 361 CGDNVOYAPRQLGTEPRYISDLAHTOYTFEIQAVNGVTDQSPSPFASVNTTNOA 420  
Db 383 cgdnvqfaprglgleprlyisdllahctgctfelgavngvtdqspfpfasvntlttna 442  
Qy 421 APSAVSIMHOVSTRVSTILSMQDPQPNVILDELYQYKEKELSEYNTAITSPTNTV 480  
Db 443 apsavsimhqvstrvstlswsqdpqpnvildelyqyekelnselstakspntvtc 502  
Qy 481 --GLKAGATYVFOVRAVTAAGYGRYSKMYFOTMTEAEYOTISOEKLPLITISSAAGLVF 538  
Db 503 vqnlkagctlyfvgrtarvaagrysgkmyfgtumeaeyqtsvqeklplilgssaaaglvf 562  
Qy 539 LIAVVVIAIVCN-RGFERADSEYTDKLOHYTSGHITTPGMKIYIDPFTYEDPNEAVREFA 597  
Db 563 liavvvliivcnrrrgferadseytdklqhytsghmtpgmklyidpftcyedpneavre 622  
Qy 598 KEIDISCVKIEBOYIGEGEGVCSGHLKLPGRKEIFVAIKTKSGYTEKORDFLSEASI 657  
Db 623 keidiscvkieqyigegefgevcsgnlklygkrelfvaltklksqytekqrdrfiseasi 682  
Qy 658 MGOFDHPNVIHEGVVTKSTPVMITTEFMEGSLDSFLRQNDGQFTVIOLVGMLRGIAG 717  
Db 683 mgqfcdhpnvnhlegvvtksespymltefmeagslslfirqndgqftvlgvmlrgiaag 742  
Qy 718 MKYLDMMNVHNDLAARNILVNSLVCKYSDFGLSRFLEDDTSDPTVTYALGKFPRIWT 777  
Db 743 mkyldmmnvhndlaarnilvnsnlvckysdfglrflddtsdptysalgygkfpirlwt 802  
Qy 778 APEALQYRKFTSASDVWSGIYVMEVMSYGERPYMDNTNOVYNLRBDYRLPRMDCPS 837  
Db 803 apealqyrkftsaasdvwsygiymvewmsygerpymdntnqvlnaleqyrlprmdcpn 862  
Qy 838 ALHQLMLDQWOKDRNHRKFGQIVTLDKMIKRNPSLAKAMPLSSGINLPLIDRTIPDYT 897  
Db 863 alhqimldcwqkdrnhhrpkfgqivntldkmltrpnslkamplssgynlplldrtclpdyt 922  
Qy 898 SFNTDEMLLEATIKGQYKESFPANGETSPDYVSCMMEDILRVGTYTLGHHOKKILINSIQV 957  
Db 923 sfntdewmlleatiksmykesfpaasagfctfdlvsqmtvedilrvgytlaghhqkllnsiqv 982  
Qy 958 MRAQNMQIOSEVEV 970  
Db 983 mraqnmqiosevev 995

XX WPI: 1995-215256/28.  
DR N-PSDB: AA090657.  
XX  
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
PT cancer.  
XX  
PS Claim 11: Page 71-75; 129pp; English.  
XX  
CC A cDNA clone encoding a novel variant of Eph-related protein Cdk5,  
CC Cdk5+ (AA090657), was isolated from a chick embryo library in  
CC lambda gt11. Cdk5+ protein (AAR75709) contains a 16-amino acid  
CC insertion in the juxtamembrane domain, and be a result of  
CC alternative splicing. Cdk5+ is exclusively expressed in the CNS.  
XX  
SQ Sequence 1011 AA:

Query Match 96.5%; Score 4934.5; DB 16; Length 1011;  
Best Local Similarity 94.0%; Pred. No. 0;  
Matches 930; Conservative 28; Mismatches 12; Indels 19; Gaps 3;

RESULT 7  
AAR75709 standard; Protein: 1011 AA.  
XX  
AC AAR75709;  
XX  
DT 11-NOV-1995 (first entry)  
XX  
DE Eph-related PTK Cdk5+.  
XX  
KW Cdk5+; Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;  
KW prognosis.  
XX  
OS Gallus sp.  
XX  
PN M09515375-A.  
XX  
PD 08-JUN-1995.  
XX  
PE 07-SEP-1994; 94MO-US10140.  
XX  
PR 03-DEC-1993; 93US-0162809.  
XX  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
XX  
PI Pasquale EB, Sajjadi FG;

Qy 1 LIAVEETLMDSTATATLDELGMVHPSPGWEVSGYDENMTTIRTYOYCNVFESSONMLR 60  
Db 23 liaveetlmdstataetalelgmvhnpesgwevsgydenmtlirtyocnvfeessonmlr 82  
Qy 61 TKFTRRGARHRIHEMKFSVRDCSTPSVPSCKEPFLNLYYADPDSATKTPNNMKNP 120  
Db 83 tkftrrgarhrihemkfsvrdcslpsvpsckepflnlyyadpdsatktpnnmkn 142  
Qy 121 WVKVDTIADESFSQVDLGRVNMKINTEVRSFGVSRSGFYLAPODYGGCMSLIAVRFY 180  
Db 143 wkvdtiaadesfsqvdlgrvnmkintevrsfgvsrsgfyfaypodyggcmsliavrfy 202  
Qy 181 RKCPRIIONAIOETLSGAESTSIYAARSCITANAEVDVPIKLYCNGDEWLPVIGRC 240  
Db 203 rkcpriionaiioetlsgaestsiaarscitanaevdvpiiklycngdewlpvigrc 262  
Qy 241 MCRAGEFAVNGTVCRCPCSGTEKANGDEACTHCPINSTRTEGATNCVCRGXYRADL 300  
Db 263 mcrpaysavngtvcrcpcsgtekanogdeacthcpinstrtegatncvcraxyradl 322  
Qy 301 DPLDMCTTTPSAPOAVISSVNETSLMLEWTPPRDSGREDLYYNTICKSCSGRGACTR 360  
Db 323 dpydmpctllpsapqavlsenvetslmlewtpdrdsqaredlylnllckscsgsrgacr 382  
Qy 361 CGDNVOYAPRQLGTEPRYISDLAHTOYTFEIQAVNGVTDQSPSPFASVNTTNOA 420  
Db 383 cgdnvqfaprglgleprlyisdllahctgctfelgavngvtdqspfpfasvntlttna 442  
Qy 421 APSAVSIMHOVSTRVSTILSMQDPQPNVILDELYQYKEKELSEYNTAITSPTNTV 480  
Db 443 apsavsimhqvstrvstlswsqdpqpnvildelyqyekelnselstakspntvtc 502  
Qy 481 --GLKAGATYVFOVRAVTAAGYGRYSKMYFOTMTEAEYOTISOEKLPLITISSAAGLVF 538  
Db 503 vqnlkagctlyfvgrtarvaagrysgkmyfgtumeaeyqtsvqeklplilgssaaaglvf 562  
Qy 539 LIAVVVIAIVCN-RGFERADSEYTDKLOHYTSGHITTPGMKIYIDPFTYEDPNEAVREFA 597  
Db 563 liavvvliivcnrrrgferadseytdklqhytsghmtpgmklyidpftcyedpneavre 622  
Qy 598 DEPTTYEDPNEAVREFAKEIDISCVKIEBOYIGEGEGVCSGHLKLPGRKEIFVAIKTKS 641  
Db 623 dpytiedpneavrefakeidiscvkieqyigegefgevcsgnlklygkrelfvaltklks 682  
Qy 642 GYTEKORDFLSEASIMGOFDHPNVIHEGVVTKSTPVMITTEFMEGSLDSFLRQNDGQ 701  
Db 683 gytেকordfllseasimgofdhpnvnhlegvvtksespymltefmeagslslfirqndgq 742  
Qy 702 FTVIOLVGLKGIAGMKYLDMMNVHNDLAARNILVNSLVCKYSDFGLSRFLEDDTSD 761  
Db 743 ftvilvgmlrgiaagmkyladmmnvhndlaarnilvnsnlvckysdfglrflddtsd 802

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QY 762 PRTYSALGKFPRTAPPAEIOVRKFTSADVSYGVAMVMSYGERPYMDTNDQVIN 821
DB 803 PLYTSALGGKIPRTWAPPAEIQKFTSADVSYGVAMVMSYGERPYMDTNDQVIN 862
QY 822 AIDQDRLRPPMDCPALHQLMDQKDRNHRKFGQIVNTLDKMI RNPNSIKAMAPLS 881
DB 863 AIEGQYRLEPPMDCPALHQLMDQKDRNHRKFGQIVNTLDKMI RNPNSIKAMAPLS 922
QY 882 SGINULPLDRTIDYTSFNVDLELAIKMGYKESFANAGFSPVVSQMMEDILRAG 941
DB 923 SGYNLPLDRTIDYTSFNVDLELAIKMGYKESFANAGFSPVVSQMMEDILRAG 982
QY 942 VTLAGHOKIINSIQVRAQMOIQSVYEV 970
DB 983 VTLAGHOKIINSIQVRAQMOIQSVYEV 1011

RESULT 8
AAR44513
ID AAR44513 standard; Protein; 984 AA.
AAR44513:
AC AAR44513:
DE 16-JUN-1994 (first entry)
XX elk.
XX
XX Lambda gtl1: expression vector; lambda-BI-Elk: protein tyrosine kinase;
KW Elk; BI: Eph; subfamily; receptor-like tyrosine kinase; eph: eck;
KW phosphorylation; phosphorylated kinase insert domain; growth factor;
XX receptor kinase; platelet-derived growth factor receptor.
XX
XX Rattus rattus.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..17 /note= "Signal peptide"
FT MISC-difference 61 /note= "Cysteine residue"
FT MISC-difference 96 /note= "Cysteine residue"
FT MISC-difference 106 /note= "Cysteine residue"
FT MISC-difference 183 /note= "Cysteine residue"
FT MISC-difference 196 /note= "Cysteine residue"
FT MISC-difference 225 /note= "Cysteine residue"
FT MISC-difference 240 /note= "Cysteine residue"
FT MISC-difference 253 /note= "Cysteine residue"
FT MISC-difference 255 /note= "Cysteine residue"
FT MISC-difference 267 /note= "Cysteine residue"
FT MISC-difference 270 /note= "Cysteine residue"
FT MISC-difference 284 /note= "Cysteine residue"
FT MISC-difference 287 /note= "Cysteine residue"
FT MISC-difference 301 /note= "Cysteine residue"
FT MISC-difference 303 /note= "Cysteine residue"
FT MISC-difference 319 /note= "Cysteine residue"
FT MISC-difference 360 /note= "Cysteine residue"
FT MISC-difference 363 /note= "Cysteine residue"

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FT /note= "Cysteine residue"
FT MISC-difference 370 /note= "Cysteine residue"
FT MISC-difference 373 /note= "Cysteine residue"
FT Modified-site 425..427 /note= "N-glycosylation site"
FT Modified-site 480..482 /note= "N-glycosylation site"
FT CA2083521-A.
FT 01-OCT-1993.
FT 23-NOV-1992; 92CA-2083521.
FT 31-MAR-1992; 92US-0861390.
FT (MOUN ) MOUNT SINAI HOSPITAL CORP.
FT Letwin K, Pawson A, Reedijk M;
FT WPI; 1993-406300/51.
FT N-PSDB; Q753471.
FT Expression of phosphorylated exogenous protein - in host cells
FT transformed with two vectors, one for the protein, the other for
FT catalytic domain of protein kinase
FT Disclosure; Fig 3; 53pp; English.
XX This sequence is encoded by the elk cDNA and represents the protein
XX tyrosine kinase, Elk. The Elk gene, BI, encode a protein which is
XX a member of the eph subfamily of protein tyrosine kinases. The Elk
XX product is very similar to two other receptor-like tyrosine kinases,
XX eph and eck. Lambda-BI-Elk may be used in the production of
XX phosphorylated exogenous protein along with a further vector encoding
XX the desired exogenous protein. These plasmids may be used to produce
XX phosphorylated proteins in host cells which have no intrinsic capacity
XX for phosphorylation, eg. bacteria. The system may be used for the
XX expression of the phosphorylated kinase insert domain of a growth
XX factor receptor kinase eg. platelet-derived growth factor receptor.
XX
XX Sequence 984 AA:
SQ
Query Match 76.4%; Score 3906.5; DB 14; Length 984;
Best Local Similarity 73.9%; Pred. No. 3.3e-285;
Matches 716; Conservative 128; Mismatches 122; Indels 3; Gaps 2;
QY 2 LAAVEETIMDSTATAELGMMVHPPSGWEVSGYDENMNTIRTYOVYCNVPESQNNMLRT 61
DB ::::|||||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||: 74
QY 62 KPIRRRGARHIVEMKFSVNDCCSISVPSCKETNIVYEDPFSAVKTPNNMENPM 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 134
QY 75 flltrgahrlyemrftvdcslpnyvpscketlnlyyecdsviatkksafseapy 134
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 194
QY 122 VKVDITIADESFSQVDLGGHVMKINTEVRSGFVSRSGLYLAFOYGGCSLIAVAVFYR 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 194
QY 182 KCPRIIONGAIFQETLSGASTSLVAARGSCIANAEVDPVPIKLYCNGOGEMLVPIGRCM 241
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 254
QY 195 kcpelvgnafvfpelmtgaestsivlariclpnaeevdvplikyncngdgmwvpiqrct 254
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 301
QY 242 CKAFEAVENGTVQFGSGPGRFANOGDEACTHCPINSRTSGATNCVCRNGYRADLD 301
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 313
QY 255 ckagyp-ensvackacpagtckasgeagcsncpsnrsrpsaplctortygyradfd 313
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 361
QY 302 PLDMPCCTTIPSAQAVAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSGSGRGACTRC 361
DB ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 373
QY 314 pvevactsvpsgrvnisvnetstlilewppretelgrdvtnylickckradsrscsc 373
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 362 GDNVQAPROGLTEPRITISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTTNGAA 421  
DB 374 ddvvefvrpqglglecrvalssaiwhatpctfdqingnsakspapqhvsnltcngaa 433  
QY 422 PSASVIMHOVSRTVDSITLSMSQPOPNVIIDELQYVEKLSFNATATSPNT--V 479  
DB 434 psrvplmbvsaclmslilswpqbepqnglildyelttyekhefnssmarsqfntarl 493  
QY 480 TGLKAGATVFOVRTAVAGRYSGKMYFQTMTEAYQTSIOEKPLITIGSSAGLVFL 539  
DB 494 dgrlprgmyvvrartvtagygkfsgkmsfgcltdddykselrrelpllagsaaqvfvf 553  
QY 540 IAVVVAIVCNRRGFERADSEYTDKLOHTSGHITPGMKIYIDPPTYEDPNEAREFAKE 599  
DB 554 vslvalsvcarckrayksaavysdklqhsytlgrspgmkiyldpfctydpneavrefake 613  
QY 600 IDISCVKIEQVIGAGEFGECVSGHLKPGKREIFAIVKITSGYTEKORROPLSFASIMG 659  
DB 614 ldsfvkleevlgagdfgevykgrlklpkrrelvalklkagysckqrdflsaasimg 673  
QY 660 QTDHPNVHLEGVVTKSPVMTTEFMENGLDSFLRONDGQFTVIOLVGMRLGIAAGMK 719  
DB 674 qtdhpnllrllegvvtcksrpvmlltefmengaldsflrqnldgqfctvlgvmlrglaagmk 733  
QY 720 YIADNNVYHROLAARNILVNSLVCKVSDFCGLSFLLEDTSDPYTTSLAGKFPRIWTAP 779  
DB 734 ylsennmyhrdlaarnilvnslyckvsdfglstrylqddtsdpclytslsgkklpvrwtap 793  
QY 740 EAIQYRKFTSADVWSYGVIMVEMVSYGERPYMDTNDVINAIEODYRLRPPMDCPAL 839  
DB 794 eaiyrfkltasadvwsyglvmewmsfgerpyvdmnsqdvlnaleqdyrlppmdcpaal 853  
QY 840 HOLMADCKQORBNRPKGGQIVNTLDKMI RNPNLSLKAMAPLSSGINDPLDRTIPDYTSF 899  
DB 854 hqlmldcwqckdrnprfaelivntldkmlrnpaslkvalitvapsqplldrsipdtaf 913  
QY 900 NTVDEMLFAIKMGQKESFANAGFTSPDVYSOMMEIOLRAGVTLAHOXKILNSIOVMR 959  
DB 914 ctvdvwlaklmvgvtrdflcagfctslqvlctqmsedllrlgvlclagqkklslsslmr 973  
QY 960 AQMNQIOGV 968  
DB 974 vqmqnspav 982

RESULT 9  
AAR75704  
ID AAR75704 standard; Protein: 951 AA.  
XX  
AC AAR75704;  
XX  
DT 11-NOV-1995 (first entry)  
XX  
DE Eph-related CEK6.  
XX  
KM Cck6; Eph: protein tyrosine-kinase; PTK; cancer; diagnosis;  
XX  
XX prognosis.  
XX  
OS Gallus sp.  
XX  
FH Key Location/Qualifiers  
FT Domain 426..444  
XX /label= Extracellular\_domain  
PN W09515375-A.  
XX  
XX  
XX 08-JUN-1995.  
XX  
XX 07-SEP-1994; 94WO-US10140.  
XX  
XX 03-DEC-1993; 93US-0162809.  
XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.  
XX  
PI Pasquale EB, Sejtadi FG;  
XX  
DR WPI: 1995-215256/28.  
XX  
PT N-PSDB: AAO90652.  
XX  
PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
XX  
PS cancer.  
XX  
PS Claim 12; Page 37-41; 129pp; English.  
XX  
XX  
XX Novel Eph-related PTK Cck6 cDNA clones (AAO90652) were isolated from  
XX chick embryo and embryonic brain cDNA libraries in phage lambda gt11.  
XX The encoded Cck6 protein (AAR75704) is closely related to rat Elk,  
XX Cck5 (AAR75712) and Cck10 (AAR75708). Cck6 transcripts were found in  
XX 10-day embryos and in adult brain, lung, heart and skeletal muscle.  
XX  
SQ Sequence 951 AA;

Query Match 72.3%; Score 3698.5; DB 16; Length 951;  
Best Local Similarity 70.1%; Pred. No. 1.4e-269;  
Matches 686; Conservative 120; Mismatches 118; Indels 55; Gaps 4;

7 ETLMDSFTTATAEIGMMVHPSPGMEVSGYDENMNTIRTYOVGVNPFSSQNNMLRTKFFIR 66  
DB 1 etlmdtlttaaelgyvtanpyswevsgydenlntlrvyvcvntepnqnnvlltflnr 60  
QY 67 RGAHRLHVEKKFSVRDCCSIPVSGCKETFNLYYEADFDSATKTFPMNMENPVKVD 126  
DB 61 rgharlrlytemrfvrdccslnpvgscetfnlyyywidsvaltkksafvteapylkvdt 120  
QY 127 IADDESQVDGGRVWKINTEVRSRSGFYLAFDYGGCSLAVRVYRKCPRI 186  
DB 121 iaadesfsqvdggrlwmk-----gffkcpav 147  
QY 187 IONGAIFQETLSGAESESTVAAAGSCIANAEVDPYIKLYCNGDGEWIVPIRCCKXGF 246  
DB 148 vqfalfpelmgaestsaltvartgclpnaeevdpiklycngdgewmvplvrcckxgy 207  
QY 247 EAVENGTVCRCPSGTFKKNQGDCACTHCPINSRTTSEGATNCVCRNGYRADLPDMP 306  
DB 208 ep-ennvactrcpactgfkasgagjlcacrpnsraesaaplccacnryftradlprcaa 266  
QY 307 CTTPSPQAVISVNETSLMLKMPPRDSGRREDLVYITCKSCSGRGACTRCGDNVQ 366  
DB 267 ctspspgprnvslsvnetslmlkmpprctggrddvlynlvckkcradrtacsrdhve 326  
QY 367 YAPROGLTEPRITISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTTNGAAPS 426  
DB 327 fvrpqglteprvflsslahpctfclqavngvsnkpfppqhvsnltcngaaapsv 386  
QY 427 IMHOVSRTVDSITLSMSQPOPNVIIDELQYVEKLSFNATATSPNT--V 479  
DB 387 lmbqvsatmrstlswpqbepqnglildyelttyeklscldpdsqfvgvsrpaadheey 446  
QY 468 NATATKSPNT--VTGLKAGATVFOVRTAVAGRYSGKMYFQTMTEAYQTSIOEKL 525  
DB 447 nssvartgnterlegrlprgmvyvvrartvtagygkfsgkmsfgcltdddykselrrel 506  
QY 526 PLITIGSSAGLVFLIAVVVAIVCNRRGFERADSEYTDKLOHTSGHITPGMKIYIDPFT 585  
DB 507 pllagsaaqvfvfvlsvlsvcarckrayksaavysdklqhsytlgrspgmkiyldpft 566  
QY 586 YEDPNEAREFAKEITDISCVKIEQVIGAGEFGECVSGHLKPGKREIFAIVKITSGYTE 645  
DB 567 yedpneavrefakeidvsvkleevlgagdfgevykgrlklpkrrelvalklkagysc 626  
QY 646 KQRDPLSEASIMGFDHPNVHLEGVVTKSPVMTTEFMENGLDSFLRONDGQFTVI 705  
DB 627 kqrldfseasimgfdhpnllrllegvvtcksrpvmlltefmengaldsflrqnldgqfctv 686





DT 11-NOV-1995 (first entry)  
 XX Eph-related PTK Cek10+.  
 DE  
 XX  
 KM Cek10+: Eph: protein tyrosine-kinase; PTK; cancer; diagnosis;  
 KM prognosis.  
 XX  
 OS Gallus sp.  
 XX  
 PN W09515375-A.  
 PD  
 XX 08-JUN-1995.  
 XX  
 PF 07-SEP-1994: 94MO-US10140.  
 XX  
 PR 03-DEC-1993: 93US-0162809.  
 XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 PI Pasquale EB, Sajjadi FG.  
 XX  
 XX  
 DR WPI: 1995-215256/28.  
 DR N-PSDB: AA090658.  
 XX  
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
 PT cancer.  
 PS  
 PS Claim 11; Page 78-82; 129pp: English.  
 XX  
 CC Novel Eph-related PTK cDNA clone Cek10 (given in AA090656) and a  
 CC variant clone, Cek10+ (AA090658), whose product contains a 15-amino  
 CC acid insertion in the juxtamembrane domain, were isolated from a  
 CC chick embryo library in lambda gt11. Cek10 and Cek10+ may  
 CC originate from the same gene by alternative splicing. Cek10  
 CC expression was prominent in the kidney, and to a lesser extent in  
 CC the lung.  
 XX  
 XX  
 SQ Sequence 988 AA:

Query Match 71.38; Score 3649.5; DB 16; Length 988;  
 Best Local Similarity 70.0%; Pred. No. 7.2e-266;

Matches 683; Conservatvie 120; Mismatches 144; Indels 29; Gaps 6;

QY 16 TAEIAGMNVHPSPGMEVGYDENMNTIRTVQCVNVESSQNNMLRTFIRRRGHRHIVE 75  
 DB 21 tselatwchpegyweevsydeamplrtcygvchvreaangnwlrkfflqrdvqryve 80  
 QY 76 MKFSVRDCSSIPSVPGSCKETFNLYYEADPDSATKTTPNMENPMWKVPTIADSESQ 135  
 DB 81 kftvrdcnsipnlpgecketfnlfyesdcsasanspfmtenpylkvdtlapdesfsk 140  
 QY 136 VDLGGRVWKITEVRSRSPVRSRSGFYLAFODYGGCNSLIARVRFKRCPRITIONGAIFOE 195  
 DB 141 lssg---rvntkvrstfprskngfyafqdlgacmclisvraflykksctntlagfalfpe 196  
 QY 196 TLGSAESTSLVAAGSGCIANAEEVDVPIKLXGNGDGMVPIGCMKAKAEFAVENTVC 255  
 DB 197 tllgaepsalvlapgtclpnavevsvplklycngdgemwvpgactcaagyeapamkdtgc 256  
 QY 256 RGCSSGTFKANGQDEACTHCPINSRTTSEGATNCVCNNGYRRADLPDLMPCTTIPSAPO 315  
 DB 257 qacpgpfkfskqegpcpcpnarcttagaatvcicrsffiradadpadsacsypsapr 316  
 QY 316 AVISVNETSLMLEMTPRDSGREDLVYNIICKSCSGSGACTRCGDNVQVAPROL--- 372  
 DB 317 svlanvnetalvlewsepqdagrdldllvnlvickcseverrlscrcddnvefvrqlgtl 376  
 QY 373 GLTEPRRIYIDLAAHTQYFEIOAVNGVTQSPFSPQFASVNTTNOAPSAVSIMHQS 432  
 DB 377 glterriyikvmahpptyfteiqavngisakppphfaevnltnqaeapavptmhlms 436  
 QY 433 RTVDSITLSNSQPDQNGVILDLVELOYEKE-LSEYNATRAIKSPNTV--TGKAKAIVV 489

DB 437 stgnsmclswcprrpnylllyelkysekqgvgdglantvscsknsvrldgllkanarym 496  
 QY 490 FOVARRTAVAGRYSGKRYFQJMTAEAYOTSIQKPLPIISSAAGVFLAVAVIIVC 549  
 DB 497 qvvarvtagrygyrlpfeftlaedgstktfqlpivysatagllfvlvvlavlc 556  
 QY 550 NRRCF-----ERADSETDKLQHTYSGHTIPGMKIYIDPFTYEDPNEAVR 594  
 DB 557 frkgmvtelqllspslgrkgrnstdpeyleklqgy-----vcpgmkyldpfyedpneavr 612  
 QY 595 EFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGRREIFAIAIKTKSGYENKORPDLSE 654  
 DB 613 efakeidiscvkieevigagefgevcgrklpgrrelfvalklkvytergrdtlfe 672  
 QY 655 ASIMGQDPHNVHLEGVVTKSTPVMITTEPMENGSLDSEFLRQNDGQFTYIQLVGMRLGT 714  
 DB 673 asimgqfthpnlhlegvvtksrprwlltefmencaidsflrlndgqfvtqlvgmrlgtl 732  
 QY 715 AAGMKYLADNMYVHRDLAARNILVNSNLCKVSDFGLSRLEDDTSDPYTTSALGKFP 774  
 DB 733 aagmkylsemnyvhrdlaarnllvnsnlckvsdfglstrleddpdpctysalggkfp 792  
 QY 775 RWTAPRALIQRKFTSASDVNSYGIWMMEVASYGERPYMDWTNDQVINAIRQDRLRPPMD 834  
 DB 793 rwtapealrkykftsasdvwsyglwmvmsygerpywmsngdvlnaveqdyrlppmd 852  
 QY 835 CPESALHOLMLDCKQKDNHRRKFGQIVNTLDKMRNPNSLKAPLSSGINTPLDRTIP 894  
 DB 853 cpelhlmlldckwvrrdtnlprkfaqlvntldklirnaaslkvlavsgvsgplldrtyp 912  
 QY 895 DYTSFNVDDEMLAIKKQYKESFANAGFTSPVVSOMMEEDILRGVTLAGHOKKILNS 954  
 DB 913 dytsfnvdemlaikqykesfanagftspvvsommeeedilrgvtlaghnqkkliss 972  
 QY 955 IOVRAQMOIQOSVEV 970  
 DB 973 iqdmrlqmqlpivgy 988

## RESULT 12

ID AAR51899 standard; Protein; 990 AA.

XX AAR51899;

DT 09-NOV-1994 (first entry)

DE Human embryonal kinase 2 receptor.

KW Embryonal kinase; HEK; protein tyrosine kinase; PTK; tumour;

KW cancer; therapy; amplification; primer; polymerase chain reaction;

OS Homo sapiens.

PN DE4233782-A.

PD 14-APR-1994.

PF 07-OCT-1992; 92DE-4233782.

PR 07-OCT-1992; 92DE-4233782.

PA (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.

PI Holtrich U, Ruebsamen-Waligmann H, Streibhardt K;

DR WPI: 1994-127194/16.

DR N-PSDB: AA062461.

PT Human embryonal kinase 2-receptor protein - useful in tumour  
 diagnosis and therapy

XX Claim 1: Page 7-10; 11pp; German.  
 CC RNA from human embryonic tissue was isolated. With the use of  
 CC primer P6(4) PK-specific cDNA was synthesized. The cDNA was  
 CC amplified using primers P6(4) and N5. A 2097 bp DNA fragment was  
 CC obtained. Primers E3, P12 and E6 were then used in the isolation of  
 CC the C-terminal of the HEK2 receptor gene.

XX Sequence 990 AA;

Query Match 70.8%; Score 3622.5; DB 15; Length 990;  
 Best Local Similarity 70.4%; Pred. No. 7.8e-264;  
 Matches 684; Conservative 114; Mismatches 159; Indels 15; Gaps 6;

QY 4 AVEETLMDSTTTAAELGAMVHPSPGMEVSGYDENMNTIRTYOVAVFESSONNLTKE 63  
 DB 29 aleetlmdtktwtselawtshpesgweevsgydeampirlygvctvressgnwltlqf 88  
 QY 64 IRRGCAHIVEKESFVSDSSIPVSGCKETPNLYYEADDSATKTPPNMNPWVK 123  
 DB 89 Iwrtvdvgrvvelkftvdcslpnlpyscketfnlfyeaadsasaspfmenpyvk 148  
 QY 124 VDTIADESFQVDLGGKVKINTEVRSFGPVSRSGFTYLAFOYDGCMSLIANRVETKRC 183  
 DB 149 vdtiapdesferidag----rvnktrsfgrlaskagfylaftgdqgacmslsvratlykcc 204  
 QY 184 PRITONAIQETLSGAESESTVAARGSCIANAEVDVPIKLYCNGDGEWLVIGRCMK 243  
 DB 205 astagallipeltlgepslviapgtclpnavevplkljcnngdgemwvpygactca 264  
 QY 244 AGFEAVENGTVCRGCPGTEFKANOGDEACTHCPINRSTSEGATVCVRNGYTRADIDL 303  
 DB 265 tghpeakesgcrcpogpsykakgqpcplpnpsrtspaaicctchnfyvadsda 324  
 QY 304 DMPCTTPSAQAQVIASSVNETSLMEWTPPRDSGREDIVYNIITCKSC--GSGRGACTRC 361  
 DB 325 dsactvpsprgyvsnvetsllwseprdlvrdillynvckckhagaggaacarc 384  
 QY 362 GDNVOYARQGLTEPRYIYISDLAHTQYFPIQAVNGVTDQSPFSPOFASVNTTNOAA 421  
 DB 385 ddnvefvrpqjseprhthllahtrctflevagovgskplpryaavnltnqaa 444  
 QY 422 PSVASIMHOSRVTDSTLSSQDPQNGVILDELOYEKELESEYNATATKSTNV-- 479  
 DB 445 psevptllhsssgslslswapperpugvilldyemkyfex--segiasvtlvsqmsvql 502  
 QY 480 TGLKAGAIYVQVBARVAGRGYSGKMYFQMTTE--AEYQTSIOEKPLILIGSSNAGLVE 538  
 DB 503 dglrpdarlvvqvartlvagygysrpfefetseersgagqldeqplrvigsataglvf 562  
 QY 539 LIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHITPQMKIYIDPFYEDNEAVREFAK 598  
 DB 563 vvavvialvcltrkqthrsdseyleklygy----lapgmkyldpftychdneavretak 618  
 QY 599 ELDISCVKTEQYIAGGEGEVCSGLKLPGKREIVATKTLKSGYTEERORDFLSEASIM 658  
 DB 619 eildvscvkleevlgagelgevcgrfklqpgvirevtaaktlkvyleteqrridflseasim 678  
 QY 659 GOFDHPNVITHLEGVYVTKSTPVMIIIEFENGSLDSFLRQNDQFTVIOVLGMRGIAAGM 718  
 DB 679 gqfdhpnllrllegvltksrpnmllefenencaldsflrlndqfvlvlgvmrlrglaagm 738  
 QY 719 KYIADNMYVHRDLAARNILVNSNLVCKYSDRFLSDPDDTSDPRTYALGSKPPIRMFA 778  
 DB 739 kyisemmyhrdlarnilvnsnlvckysdrlsflleddpsdprtytslsgkplrvta 798  
 QY 779 PEATQYRKRTSADWVSYSIVMMEVSYSGERPMDTMDTNAINALEODYRLPPEPMDCSA 838  
 DB 799 peiaiyrkrtssadwvsyivmmevsgygerpywmsngdvlnavegdyrlrppmdcpta 858  
 QY 839 LHOJLMDCWQKQNRHPRKFGQIVNTLDDKMIIRNPNSLIKAMAPLSSGINPLDRTITPDTYS 898

DB 859 lhgimldcwvtrdnrlrbyfsqivntlkilnaaslkvisasagmsqplldctypdytt 918  
 QY 899 FNTVDENLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRVGYTLAGHOKTILNSIQVA 958  
 DB 919 ftrvgdwldakmgrykesfvsagfasfdlvaqntaedllrvtytlagbhkklissyqdm 978  
 QY 959 RAQNMQIOSVEY 970  
 DB 979 rlgmqnqlrpqv 990

# RESULT 13

AAR75843  
 ID AAR75843 standard; Protein: 993 AA.

AA75843;  
 24-NOV-1995 (first entry)

Protein p140 CDNA from rat skeletal muscle myoblast cell line L6.

Protein p140; insulin; tyrosine phosphorylation.

Rattus rattus.

EP659883-A.

28-JUN-1995.

24-NOV-1994; 94EP-0118524.

PR 24-NOV-1993; 93JP-0315806.

(ONOR ) ONO PHARM CO LTD.

Kitagawa K, Ohno H, Tajima H;

WPI; 1995-226291/30.

Isolated protein p140 polypeptide - and treatment of diabetes based

on tyrosine phosphorylation of protein p140.

Claim 1; Page 19-23; 42pp; English.

A cDNA library was established from rat skeletal myoblast cell line

L6. DNA fragments of approx. 400 bp were recovered and subjected to

cloning. 20 plasmids were sequenced. Sequence data of cDNA fragments

were constructed to the linkage sequences with the DNA programme

DNASIS. The basic sequence portrayed in AA090972 was hence constructed.

From sequence data of the whole cDNA length, the ORF was determined.

The AA sequence was further translated and the sequence thus

established is illustrated in AAR75843. One of the frames possesses

the 2993-bp ORF, that was approximated to 3000 bp of the whole ORF

length of the Eck family. p140 is used for the prevention and

treatment of diabetes. Dosage is 10 microg-1000 mg (p.o.) or

10 microg-100mg (i.v.).

Sequence 993 AA;

Query Match 70.2%; Score 3590.5; DB 16; Length 993;

Best Local Similarity 68.4%; Pred. No. 2e-261;

Matches 679; Conservative 116; Mismatches 163; Indels 35; Gaps 7;

QY 3 AAVEETLMDSTTTATA-----ELGWMVHPSPGMEVSGYDENMNTIRTY 45

DB 11 aaaseraaaeatnslslvrtsegsrldsefvelawtshpesgweevsgydeampirly 70

QY 46 QVCNVFESSONNMLRTKFIIRKCAHRIHVEMKTSVRCSSIPVPSCKETNLYYEAD 105

DB 71 qvcnvressgnwltlrgfivrtrevgyvelkltvdcnslpnlpyscketfnlfyead 130





Wed Jul 25 13:03:56 2001

Db 959 qlmkvhlnglpev 973

Search completed: July 24, 2001, 16:28:46  
Job time: 417 sec

us-09-378-759-11.rag

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 24, 2001, 16:29:14 ; Search time 14.81 Seconds

(without alignments)  
2243.607 Million cell updates/sec

Title: US-09-378-759-11

Sequence: 1 LLAIVETLMDSTTATLGLG.....ILNSIQVRAQMNOIOSVEV 970

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5089	99.5	1055	1	EPB2_HUMAN
2	5082	99.3	993	1	EPB2_MOUSE
3	4932.5	96.4	1004	1	EPB2_CHICK
4	4902	95.8	987	1	EPB2_COTJA
5	3914.5	76.5	984	1	EPB1_RAT
6	3899.5	76.2	984	1	EPB1_HUMAN
7	3754	73.4	985	1	EPBA_XENLA
8	3704	72.4	984	1	EPB1_CHICK
9	3649.5	71.3	988	1	EPB3_HUMAN
10	3632.5	71.0	998	1	EPB3_MOUSE
11	3604	70.4	993	1	EPBB_XENLA
12	3593.5	70.2	992	1	EPBB_XENLA
13	3465.5	65.3	1002	1	EPB5_CHICK
14	3341.5	60.0	986	1	EPBA_XENLA
15	3070	59.8	985	1	EPAB_XENLA
16	3060.5	59.5	986	1	EPAB_XENLA
17	3042	59.2	986	1	EPAB_XENLA
18	3031	59.2	986	1	EPAB_XENLA
19	3026.5	59.2	986	1	EPAB_XENLA
20	3026	59.2	986	1	EPAB_XENLA
21	3016	59.0	986	1	EPAB_XENLA
22	3014	58.9	986	1	EPAB_XENLA
23	3001	58.7	986	1	EPAB_XENLA
24	3001	58.7	986	1	EPAB_XENLA
25	2990	58.4	986	1	EPAB_XENLA
26	2918.5	57.0	983	1	EPB3_HUMAN
27	2914	56.8	983	1	EPB3_CHICK
28	2904	56.8	983	1	EPB3_CHICK
29	2902	56.7	984	1	EPB3_RAT
30	2875.5	56.2	983	1	EPB3_MOUSE
31	2840.5	55.5	981	1	EPB3_BRARE
32	2835.5	55.4	987	1	EPB4_MOUSE
33	2811	54.9	1035	1	EPB6_MOUSE

## ALIGNMENTS

RESULT	ID	EPB2_HUMAN	STANDARD	PRT	1055 AA.
AC	P29323	043477			
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-OCT-2000	(Rel. 40, Last sequence update)			
DT	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	EPHRIIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-3) (DRT) (RECEPTOR PROTEIN-TYROSINE KINASE HEK5) (ERK).				
GN	EPHB2 OR EPHB3 OR ERK OR DRT OR HEK5.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).				
RC	TISSUE-Fetal brain;				
RX	MEDLINE-96154673; PubMed-8589679;				
RA	Ikegaki N., Tang X.X., Liu X.-G., Biegel J.A., Allen C.,				
RT	Yoshioaka A., Sulman E.P., Brodeur G.M., Pleasure D.E.;				
RT	"Molecular characterization and chromosomal localization of DRT				
RT	(EPH3): a developmentally regulated human protein-tyrosine kinase				
RT	gene of the EPH family.";				
RL	Hum. Mol. Genet. 4:2033-2045(1995);				
RN	[2]				
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).				
RC	TISSUE-Gastric carcinoma;				
RX	MEDLINE-93343925; PubMed-7688222;				
RA	Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;				
RT	"Identification of protein-tyrosine kinase genes preferentially				
RT	expressed in embryyo stomach and gastric cancer.";				
RT	Biochem. Biophys. Res. Commun. 194:698-705(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A. (LONG ISOFORM).				
RC	TISSUE-Fetal brain;				
RX	MEDLINE-96359217; PubMed-9696046;				
RA	Tang X.X., Pleasure D.E., Brodeur G.M., Ikegaki N.;				
RT	"A variant transcript encoding an isoform of the human protein				
RT	tyrosine kinase EPHB2 is generated by alternative splicing and				
RT	alternative use of polyadenylation signals.";				
RT	Oncogene 17:521-526(1998).				
RN	[4]				
RP	SEQUENCE OF 15-986 FROM N.A. (SHORT ISOFORM).				
RC	TISSUE-Brain;				
RX	MEDLINE-95206782; PubMed-7898931;				
RA	Fox G.M., Holst P.L., Chute H.T., Landberg R.A., Janssen A.M.,				
RT	Basu R., Welcher A.A.;				
RT	"cDNA cloning and tissue distribution of five human EPH-like receptor				
RT	protein-tyrosine kinases.";				
RT	Oncogene 10:897-903(1995).				
RN	[5]				
RP	SEQUENCE OF 509-986 FROM N.A. (SHORT ISOFORM).				
RC	TISSUE-Brain;				
RA	Saito T., Nishiko S., Kishihara M., Murata M., Yamamoto Y.,				
RA	Hori T., Matsuda Y.;				

34	2799.5	54.7	987	1	EPB4_HUMAN	P54760 homo sapien
35	2650	51.8	1004	1	EPAB_MOUSE	O09127 mus musculu
36	2600	50.8	948	1	EPAB_RAT	P54758 rattus norv
37	2446	47.8	1014	1	EPB6_MOUSE	O08644 mus musculu
38	2442	47.7	877	1	EPAS_MOUSE	O06629 mus musculu
39	2438	47.7	1006	1	EPB6_HUMAN	O15197 homo sapien
40	2349.5	45.9	976	1	EPB2_HUMAN	P29317 homo sapien
41	2340.5	45.7	977	1	EPB2_MOUSE	O03145 mus musculu
42	1905.5	37.2	976	1	EPB1_HUMAN	P21709 homo sapien
43	1648	32.2	500	1	EPB3_BRARE	O13147 brachydanto
44	1197.5	23.4	372	1	EPB8_RAT	P29321 rattus norv
45	1187.5	23.2	292	1	EPB4_BRARE	O13148 brachydanto

Submitted (Aug-1994) to the EMBL/Genbank/DBJ databases.

[6] SEQUENCE OF 652-712 FROM N.A.

RA MEDLINE-91296384; PubMed-1648701;

RT Chan J., Watt V.M.;

RT "eek and erk, new members of the eph subclass of receptor protein-tyrosine kinases.";

RT Oncogene 6:1057-1061(1991).

RL [7]

RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (SHORT ISOFORM).

RA MEDLINE-99132419; PubMed-9933164;

RT Thawes C.D., Goodwill K.E., Bowie J.U.;

RT "Oligomeric structure of the human EphB2 receptor SAM domain.";

RT Science 283:833-836(1999).

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. THE LIGAND-ACTIVATED FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-EPH2 THROUGH THE JUXTAMEMBRANE TYROSINES RESIDUES (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/EPH2V (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: BRAIN, HEART, LUNG, KIDNEY, PLACENTA, PANCREAS, LIVER AND SKELETAL MUSCLE. PREFERENTIALLY EXPRESSED IN FETAL BRAIN.

CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.

CC -----

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CC -----

DR EMBL: LA1939; AAA99310.1; -

DR EMBL: D31661; BAA06506.1; -

DR EMBL: AF025304; AAB94602.1; -

DR EMBL: D14717; BAA03537.1; -

DR EMBL: D16643; AAA74244.1; -

DR EMBL: D37827; BAA07073.1; -

DR EMBL: X59292; CAA41981.1; -

DR PDB: 1BAF; 16-FEB-99.

DR MIM: 600997; -

DR InterPro: IPR000561; -

DR InterPro: IPR000719; -

DR InterPro: IPR001090; -

DR InterPro: IPR001245; -

DR InterPro: IPR001426; -

DR InterPro: IPR001660; -

DR InterPro: IPR001777; -

DR Pfam: PF01404; EPH\_1bd; 1.

DR Pfam: PF00536; SAM; 1.

DR Pfam: PF00041; In3; 2.

DR Pfam: PF00069; Pkinase; 1.

DR PRINTS: PR00014; FNTYPEP11.

DR PRINTS: PR00109; TYRKINASE.

DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE: PS00109; PROTEIN KINASE DOM; 1.

DR PROSITE: PS00111; PROTEIN KINASE TYR; 1.

DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.

DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.

DR PROSITE: PS01186; EGF\_2; UNKNOWN; 1.

DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;

KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;

KW Alternative splicing; Repeat.

KW SIGNAL

FT CHAIN 1 18 POTENTIAL.

FT SIGNAL 19 1055 EPHRIN TYPE-B RECEPTOR 2.

Query Match	Best Local Similarity	Score 5089; DB 1; Length 1055;
Matches 966; Conservative	2; Mismatches	1; Indels 2; Gaps 1;
1 LLAAYEETLMDSTTATAEELGMVHPSPGWEVSGYDENNTIRTYOVQNVFESSQNNMLR	99.5%; Pred. No. 0;	60
15 LLAAYEETLMDSTTATAEELGMVHPSPGWEVSGYDENNTIRTYOVQNVFESSQNNMLR	99.5%; Pred. No. 0;	74
61 TKFIRRRGAHRIHVEKFSYVROCSSITPSYPGSGCKETFNLYYEADFDSDATKTFPMNMENP	99.5%; Pred. No. 0;	120
75 TKFIRRRGAHRIHVEKFSYVROCSSITPSYPGSGCKETFNLYYEADFDSDATKTFPMNMENP	99.5%; Pred. No. 0;	134
121 WVKVDITIADESFQVDLGGKRVKINTEVRSFGVPSRSFGYLAFODYGGCMLIAVRFY	99.5%; Pred. No. 0;	180
135 WVKVDITIADESFQVDLGGKRVKINTEVRSFGVPSRSFGYLAFODYGGCMLIAVRFY	99.5%; Pred. No. 0;	194
181 RKCPRITIQNGAIFQETILSGAESTSLVAARSGCIANAEVDVPLIKLXCNDDGEMIVPIGRC	99.5%; Pred. No. 0;	240
195 RKCPRITIQNGAIFQETILSGAESTSLVAARSGCIANAEVDVPLIKLXCNDDGEMIVPIGRC	99.5%; Pred. No. 0;	254
241 MCKAGFAVNGTVCGPCGPGTFKANGDCACTHGINSTTSEGATNCVCRNGYRADL	99.5%; Pred. No. 0;	300
255 MCKAGFAVNGTVCGPCGPGTFKANGDCACTHGINSTTSEGATNCVCRNGYRADL	99.5%; Pred. No. 0;	314
301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLYNITICSGSGGRACR	99.5%; Pred. No. 0;	360
315 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLYNITICSGSGGRACR	99.5%; Pred. No. 0;	374
361 CGDNVQYAPRQGLGTERITISDLAHTOYTFEIOAVNGVTDOSPSPQFASVNTITNQA	99.5%; Pred. No. 0;	420
375 CGDNVQYAPRQGLGTERITISDLAHTOYTFEIOAVNGVTDOSPSPQFASVNTITNQA	99.5%; Pred. No. 0;	434



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OY 421 APSAVSIMHOVSRVDSITLSHSPDQPCNGVILIDELQYIEKLESEYNATAIKSPNTVT 480
D 435 APSAVSIMHOVSRVDSITLSHSPDQPCNGVILIDELQYIEKLESEYNATAIKSPNTVT 494
OY 481 --GLKAGAIYVFOVRATVAGYGRYSCKMYFOTMTEKEVOTSIQELPLITISSAGLVF 538
D 495 VQGLKAGAIYVFOVRATVAGYGRYSCKMYFOTMTEKEVOTSIQELPLITISSAGLVF 554
OY 539 LIAVVAIATCNRRGFRADSETDKLOHYSCHITPGMKIYIDPPTYEDPNEAREFAK 598
D 555 LIAVVAIATCNRRGERADSETDKLOHYSCHITPGMKIYIDPPTYEDPNEAREFAK 614
OY 599 EIDISCKIEOVIGAGEFEGVCGHKLPGKREIFAATITLKSGETEKORPFLSEASIM 658
D 615 EIDISCKIEOVIGAGEFEGVCGHKLPGKREIFAATITLKSGETEKORPFLSEASIM 674
OY 659 GQPDHENVHLEGVVTKSPVMTTEFEMENGSLDSFLRONDOQFTVIOLVGLRGIAAGM 718
D 675 GQPDHENVHLEGVVTKSPVMTTEFEMENGSLDSFLRONDOQFTVIOLVGLRGIAAGM 734
OY 719 KYLADNNVYHRLAARNILVNSNLCKVSDGLSRFLSDPTTYSALGKPIRMTA 778
D 735 KYLADNNVYHRLAARNILVNSNLCKVSDGLSRFLSDPTTYSALGKPIRMTA 794
OY 779 PEAIQYRKFTSASDVMSYGVIMMEVMSYGERPYMDTQDVINAIEODYRLPPMDQCSA 838
D 795 PEAIQYRKFTSASDVMSYGVIMMEVMSYGERPYMDTQDVINAIEODYRLPPMDQCSA 854
OY 839 LHOQLMDCQKORNRHPRFGQVNTLDMKIRNPNSLKMADPLSSGILNPLDRTIPYTS 898
D 855 LHOQLMDCQKORNRHPRFGQVNTLDMKIRNPNSLKMADPLSSGILNPLDRTIPYTS 914
OY 899 FNTVDEMLEAIKMGQKESFANAGTSPDVYSOMMEDILVGTGLGHOKKILNSIQVM 958
D 915 FNTVDEMLEAIKMGQKESFANAGTSPDVYSOMMEDILVGTGLGHOKKILNSIQVM 974
OY 959 RAOHQIOISVE 969
D 975 RAOHQIOISVE 985

RESULT 2
ID EPR2_MOUSE STANDARD: PRT: 993 AA.
AC P54763; 062213;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR EPH-3) (NUK) (SEK-3) (FRAGMENT).
GN EPHB2 OR EPH3 OR NUK OR SEK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Henkemeyer M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 515-993 FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=95034306; PubMed=7947319;
RA Becker N., Selandidou T., Murphy P., Mattei M.-G., Topilko P.,
RA Nieto A., Wilkinson D.G., Charney P., Gialardi P.;
RT "Several receptor tyrosine kinase genes of the Eph family are
RT segmentally expressed in the developing hindbrain.";
RL Mech. Dev. 47:3-17(1994).
RN [3]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors

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RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.*;
RL Development 127:1397-1410(2000).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. CAN
CC FUNCTION IN ASPECTS OF RETINAL GANGLION CELL AXON GUIDANCE TO THE
CC OPTIC DISK EVEN LACKING ITS TYROSINE KINASE DOMAIN. THE LIGAND-
CC ACTIVATED FORM INTERACTS WITH MULTIPLE PROTEINS, INCLUDING GTPASE-
CC ACTIVATING PROTEIN (RASGAP) THROUGH ITS SH2 DOMAIN. RASGAP BINDS
CC EPHB2 THROUGH THE JUXTAMEMBRANE TYROSINE RESIDUES (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE DEVELOPING OUTER
CC RETINA.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L25890; AA7241.1; ALT_INT.
DR EMBL: X76011; CAA53598.1; -.
DR HSSP: P00523; 2PTR.
DR MGD: MG1:99611; Ephb2.
DR InterPro: IPR000561; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001090; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001426; -.
DR InterPro: IPR001660; -.
DR InterPro: IPR001777; -.
DR Pfam: PF01404; EPH_Lbd; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; PKinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V2; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT NON_TER 1
FT SIGNAL <1 25
FT CHAIN 26 993
FT DOMAIN 26 550
FT TRANSMEM 551 571
FT DOMAIN 572 993
FT DOMAIN 191 328
FT DOMAIN 329 438
FT DOMAIN 439 536
FT DOMAIN 628 891
FT DOMAIN 918 993
FT SITE 991 993
FT NP_BIND 634 642
FT BINDING 660 660
FT ACT_SITE 753 753
FT MOD_RES 603 603
FT MOD_RES 609 609
FT MOD_RES 787 787
FT MOD_RES 937 937
FT CARBOHYD 272 272
FT CARBOHYD 343 343
FT CARBOHYD 435 435
FT -----
FT POTENTIAL.
FT EPHRIN TYPE-B RECEPTOR 2.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT CYS-RICH.
FT FIBRONECTIN TYPE-III.
FT FIBRONECTIN TYPE-III.
FT PROTEIN KINASE.
FT SAM.
FT PDZ-BINDING MOTIF (POTENTIAL).
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.
FT PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 575 575 R -> RR (IN REF. 2).  
 SO SEQUENCE 993 AA: 110628 MW: A0E1A695F46587E8 CRC64;

Query Match 99.3%; Score 5082; DB 1; Length 993;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

1 LLAAVEETLMDSTTATVAELGMVHPSPGNEEVSGDENMNTIRITVOCVNVESSONMLR 60  
 22 LLAAVEETLMDSTTATVAELGMVHPSPGNEEVSGDENMNTIRITVOCVNVESSONMLR 81  
 61 TKIRRGARHIVEKFSVRCOSSIPSPGSKETENLYTEADPDSATKFPMMENP 120  
 82 TKFIRRGARHIVEKFSVRCOSSIPSPGSKETENLYTEADPDSATKFPMMENP 141  
 121 WVKVDTIADESESOYDLGGRVAKINTEVSRFGVSRSGFYLAPODYGGCMLIAVRFY 180  
 142 WVKVDTIADESESOYDLGGRVAKINTEVSRFGVSRSGFYLAPODYGGCMLIAVRFY 201  
 181 RCPRIITQCAITOEITLSCAESTSLVAARSGCTANAEVDVPIKLYCNGDGEMLVIGRC 240  
 202 RCPRIITQCAITOEITLSCAESTSLVAARSGCTANAEVDVPIKLYCNGDGEMLVIGRC 261  
 241 MCRAGFEAVENGTCVRCGCPGCTFKANGDEACTHCPINSTRTSEGATNCVRNGYRADL 300  
 262 MCRAGFEAVENGTCVRCGCPGCTFKANGDEACTHCPINSTRTSEGATNCVRNGYRADL 321  
 301 DPLDMPCTTIPSAFOAVISSVNETSLMLEWTPPRDSGREDLYNITICSGSGRGACTR 360  
 322 DPLDMPCTTIPSAFOAVISSVNETSLMLEWTPPRDSGREDLYNITICSGSGRGACTR 381  
 361 CGDVOVYAPRGLGTEPRITISDLAHTOYTFEIOAVNGYTDOSPSPASVNTITNOA 420  
 382 CGDVOVYAPRGLGTEPRITISDLAHTOYTFEIOAVNGYTDOSPSPASVNTITNOA 441  
 421 APSAVSIMHOVSRTVDSTLTSWSPDPDPNGVILDELOYYEKELESEVNAITKSPNTVT 480  
 442 APSAVSIMHOVSRTVDSTLTSWSPDPDPNGVILDELOYYEKELESEVNAITKSPNTVT 501  
 481 --GKAGAIYVFOYARAVAGYGRSGKMPQMTAEAYOTSIOEKLPLITIGSSAGLVF 538  
 502 VOGKLAGAIYVFOYARAVAGYGRSGKMPQMTAEAYOTSIOEKLPLITIGSSAGLVF 561  
 539 IIAVVVIAIVCNRGFEADSEYTDKLOHTSGHITPGMKIYIDPFYEDPNEAVREFAK 598  
 561 IIAVVVIAIVCNRGFEADSEYTDKLOHTSGHITPGMKIYIDPFYEDPNEAVREFAK 621  
 599 EIDISCVRIEYOYIGAGEGECVSGHLKPGKREIFVAIKTLKSGYTEKORRDFLSEASIM 658  
 622 EIDISCVRIEYOYIGAGEGECVSGHLKPGKREIFVAIKTLKSGYTEKORRDFLSEASIM 681  
 659 GOFDPBNVTHLEGVYTKSPVMIITEFMEGNSLDSFLRQNDGQFTVIQVLMLRGIAAGM 718  
 682 GOFDPBNVTHLEGVYTKSPVMIITEFMEGNSLDSFLRQNDGQFTVIQVLMLRGIAAGM 741  
 719 KVLADNVVHRDLAARNILVNSNLVCKYSDRGLSRFLDDPISDPYITSLGKPIRMTA 778  
 742 KVLADNVVHRDLAARNILVNSNLVCKYSDRGLSRFLDDPISDPYITSLGKPIRMTA 801  
 779 PEALIOYRKFTSADVWSYGIIVMEVWSYGERPYMTNDVINAIEODYRLPPMDCSA 838  
 802 PEALIOYRKFTSADVWSYGIIVMEVWSYGERPYMTNDVINAIEODYRLPPMDCSA 861  
 839 LHOJLMDCKQKDRNHRPKFGQIVNTLDMKIRNPNLSIKAMAPLSSGGINPLDRTIPDYS 898  
 862 LHOJLMDCKQKDRNHRPKFGQIVNTLDMKIRNPNLSIKAMAPLSSGGINPLDRTIPDYS 921  
 899 FNTVDEMLAIKMGQYKESFANAGTSPDVVSOMMEDILRIGVTLTAGHOKKILNSIOVM 958  
 922 FNTVDEMLAIKMGQYKESFANAGTSPDVVSOMMEDILRIGVTLTAGHOKKILNSIOVM 981

QY 959 RAOMNOIOSVEV 970  
 Db 982 RAOMNOIOSVEV 993

RESULT 3  
 EPH2\_CHICK  
 ID EPH2\_CHICK STANDARD; PRT; 1004 AA.  
 AC P28693;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-OCT-2000 (Rel. 40, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
 DE KINASE RECEPTOR CEK5).  
 GN EPHB2 OR CEK5.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 CX NCBI\_TaxID=9031;  
 RN (1)  
 RN SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RP TISSUE-Embryo;  
 RX MEDLINE=92144672; PubMed=1664238;  
 RA Pasquale E.B.;  
 RT Identification of chicken embryo kinase 5, a developmentally  
 RT regulated receptor-type tyrosine kinase of the Eph family.";  
 RL Cell Regul. 2:523-534(1991).  
 RN (2)  
 RN SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).  
 RP TISSUE-Brain;  
 RX MEDLINE=93288394; PubMed=8510926;  
 RA Sajjadi F.G., Pasquale E.B.;  
 RT "Five novel avian Eph-related tyrosine kinases are differentially  
 RT expressed".  
 RL Oncogene 8:1807-1813(1993).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN  
 CC -1- IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC -1- PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/CEK5+ (SHOWN HERE)  
 CC -1- AND A SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT  
 CC -1- DEVELOPMENT AND SPECIALLY EXPRESSED IN THE CENTRAL NERVOUS  
 CC -1- FORM (CEK5+) IS SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS  
 CC -1- SYSTEM.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC -1- RECEPTOR SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M62325; AAA48667.1; ALT\_INIT.  
 CC HSSP: P00523; 2PTK.  
 DR InterPro: IPR000561;  
 DR InterPro: IPR000719;  
 DR InterPro: IPR001090;  
 DR InterPro: IPR001245;  
 DR InterPro: IPR001245;  
 DR InterPro: IPR001426;  
 DR InterPro: IPR001660;  
 DR InterPro: IPR001777;  
 DR Pfam: PF01404; EPH\_1bd; 1.  
 DR Pfam: PF00536; SAM\_1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pkinase; 1.

DR PRINTS: PRO00104; ENTYPETIT.  
 DR PROSITE: PS00107; TYRKINASE.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP\_1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR\_1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_DOM\_1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1\_1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2\_1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 DR Transferrase; tyrosine-protein kinase; ATP-binding; phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;  
 KW Repeat.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 1004 EPHRIN TYPE-B RECEPTOR 2.  
 FT DOMAIN 20 544 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 545 565 POTENTIAL.  
 FT DOMAIN 566 1004 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 20 321 CYS-RICH.  
 FT DOMAIN 326 419 FIBRONECTIN TYPE-III.  
 FT DOMAIN 437 521 FIBRONECTIN TYPE-III.  
 FT DOMAIN 639 902 PROTEIN KINASE.  
 FT DOMAIN 929 1004 SAM.  
 FT SITE 1002 1004 PDZ-BINDING MOTIF (POTENTIAL).  
 FT NP\_BIND 645 653 ATP (BY SIMILARITY).  
 FT BINDING 671 671 ATP (BY SIMILARITY).  
 FT ACT\_SITE 764 764 BY SIMILARITY.  
 FT MOD\_RES 614 614 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 620 620 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 798 798 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 948 948 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 591 606 MISSING (IN SHORT ISOFORM).  
 SQ SEQUENCE 1004 AA; 111963 MW; 8D26213970ECC6D CnC64.

Query Match Best Local Similarity 96.48; Score 4932.5; DB 1; Length 1004;  
 Matches 930; Conservative 28; Mismatches 12; Indels 19; Gaps 3;

QY 1 LLAAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMMNTIRYOCNPESSONMLR 60  
 DB 16 LLAAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMMNTIRYOCNPESSONMLR 75  
 QY 61 TKETRRRGARIRIHEMKFVSVDSSIPSVPSCKETENLYEADFPDPAKTFPMNMENP 120  
 DB 76 TKYIRRGARIRIHEMKFVSVDSSIPSVPSCKETENLYEADFPDPAKTFPMNMENP 135  
 QY 121 WVKVDTLAADSPFQVLDGKVMKINTEVSGVSSGFLAFODYGGCKSLIAVVEFY 180  
 DB 136 WVKVDTLAADSPFQVLDGKVMKINTEVSGVSSGFLAFODYGGCKSLIAVVEFY 195  
 QY 181 RKCPRITQNGAIFQETLSGAESTSLVAARSGCINAAEENVPILYCNNGGEMLVPIGR 240  
 DB 196 RKCPRITQNGAIFQETLSGAESTSLVAARSGCINAAEENVPILYCNNGGEMLVPIGR 255  
 QY 241 MCKAGFAVENGVCRGCPGSGTFKANGDEACTHCPIINSRTSGATNCVCRNQYRADL 300  
 DB 256 MCRGYESVENVGVCRGCPGSGTFKANGDEACTHCPIINSRTSGATNCVCRNQYRADL 315  
 QY 301 DPLDMPCTTIPSAPOAYISSVNEISLMEWTPPRDSSGRDLYNITCKSCGSGRACATR 360  
 DB 316 DPLDMPCTTIPSAPOAYISSVNEISLMEWTPPRDSSGRDLYNITCKSCGSGRACATR 375  
 QY 361 CGDNVQAPARQGLTEPRIRIYISDLAHTQYTFETQAVNGTDPSPSPASVNIITNOA 420  
 DB 376 CGDNVQAPARQGLTEPRIRIYISDLAHTQYTFETQAVNGTDPSPSPASVNIITNOA 435  
 QY 421 APSAVSITMHOVSRTVDSTITLSSQSDPQNGVILDELYEYKELSEYNATAIKSPNTVT 480  
 DB 436 APSAVSITMHOVSRTVDSTITLSSQSDPQNGVILDELYEYKELSEYNATAIKSPNTVT 495

QY 481 --GLKAGIYFQVARTVAGYGRYSGMYFOTTEAEYOTSIOEKPLIIIGSSAACTF 538  
 DB 496 VQNKAGIYFQVARTVAGYGRYSGMYFOTTEAEYOTSIOEKPLIIIGSSAACTF 555  
 QY 539 LIAVVAIVCN-RRGEFADSEYTKLOHYTSGH-----ITPGMKIYI 581  
 DB 556 LIAVVAIVCN-RRGEFADSEYTKLOHYTSGH-----ITPGMKIYI 615  
 QY 582 DPEFYEDPNEAVREFAEIDISCKIIOYVIGAGFEGVCGHLKPKREIFAIAIKLKS 641  
 DB 616 DPEFYEDPNEAVREFAEIDISCKIIOYVIGAGFEGVCGHLKPKREIFAIAIKLKS 675  
 QY 642 GYTEKQRDFSEASISINGOPDHPVNIHLEGVYTSFPMIITTEPMENGLSDSFLRNDGQ 701  
 DB 676 GYTEKQRDFSEASISINGOPDHPVNIHLEGVYTSFPMIITTEPMENGLSDSFLRNDGQ 735  
 QY 702 FTVIQLVGMRLGIAAGKKYLDAMNYVRDLAARNILVNSMLYCKVSDPGLSRELEDDTSD 761  
 DB 736 FTVIQLVGMRLGIAAGKKYLDAMNYVRDLAARNILVNSMLYCKVSDPGLSRELEDDTSD 795  
 QY 762 PTYSALGKFPRTWTAPEAIQYRKFTSASDWSYGIYVMEVNSYGERPYMDTNDVYN 821  
 DB 796 PTYSALGKFPRTWTAPEAIQYRKFTSASDWSYGIYVMEVNSYGERPYMDTNDVYN 855  
 QY 822 AIEODYRLPPMDCPSALHOLMDCMOKDRNHRPKFGQIVNTLDKMIIRNPNSLKAMAPLS 881  
 DB 856 AIEODYRLPPMDCPSALHOLMDCMOKDRNHRPKFGQIVNTLDKMIIRNPNSLKAMAPLS 915  
 QY 882 SGINPLPLDRTIDYTSFNTVDEMLEIAIKGOYKESFANAGFTSPVDSQMMEDILRVG 941  
 DB 916 SGVNLPLDRTIDYTSFNTVDEMLEIAIKGOYKESFANAGFTSPVDSQMMEDILRVG 975  
 QY 942 VTLAGHOKTILNSIOVRAQMOIOSEYV 970  
 DB 976 VTLAGHOKTILNSIOVRAQMOIOSEYV 1004

RESULT 4  
 EPR2\_COTUA ID EPR2\_COTUA STANDARD; PRT; 987 AA.  
 AC 090344;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR GEF5).  
 GN EPHB2 OR GEF5.  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.  
 OX NCBI\_TaxID=93934;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA MEDLINE=96109331; PubMed=8612986;  
 RX Kennedy D., Bronner-Fraser M., Marcelle C.;  
 RT "The receptor tyrosine kinase GEF5 mRNA is expressed in a gradient within the neural retina and the tectum.";  
 RL Dev. Biol. 172:708-716(1995).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.  
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EMBL: X91737; CA62862.1; -  
 DR HSPB; P00523; 2PK.  
 DR InterPro: IPR000561; -  
 DR InterPro: IPR000719; -  
 DR InterPro: IPR001090; -  
 DR InterPro: IPR001245; -  
 DR InterPro: IPR001426; -  
 DR InterPro: IPR001660; -  
 DR InterPro: IPR001777; -  
 DR Pfam: PF01404; EPH\_Lbd; 1.  
 DR Pfam: PF00536; SAM; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0014; ENTYPETIT.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; FALSE\_NEG.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE: PS0186; EGF\_2; UNKNOWN\_1.  
 DR Transferrase: Tyrosine-protein kinase: ATP-binding; phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 19  
 FT CHAIN 20 987  
 FT DOMAIN 20 544  
 FT TRAMEM 545 565  
 FT DOMAIN 566 987  
 FT DOMAIN 185 322  
 FT DOMAIN 323 432  
 FT DOMAIN 433 530  
 FT DOMAIN 622 885  
 FT DOMAIN 912 987  
 FT SITE 985 987  
 FT NP\_BIND 628 636  
 FT BINDING 654 654  
 FT ACT\_SITE 747 747  
 FT MOD\_RES 597 597  
 FT MOD\_RES 603 603  
 FT MOD\_RES 781 781  
 FT MOD\_RES 931 931  
 FT CARBOHYD 266 266  
 FT CARBOHYD 337 337  
 FT CARBOHYD 429 429  
 FT CARBOHYD 478 478  
 FT CARBOHYD 483 483  
 SQ SEQUENCE 987 AA; 110331 MW; 05D6ECC68B718DD7 CRC64;

Query Match 95.8%; Score 4902; DB 1; Length 987;  
 Best Local Similarity 94.7%; Pred. No. 1e-295;  
 Matches 920; Conservative 30; Mismatches 20; Indels 2; Gaps 1;

QY 1 LLAVEETLMDSTTATTAELGMMVPPSGMEVSGYDENMNTITTYOVCAVFESSQNNMLR 60  
 DB 16 LLAVEETLMDSTTATTAELGMMVPPSGMEVSGYDENMNTITTYOVCAVFESSQNNMLR 75  
 QY 61 TKIRIRRGARIRIVEMKFSVRDCSSIPNPGSKETFNLLYYEADDSATKTPNNMENP 120  
 DB 76 TKIRIRRGARIRIVEMKFSVRDCSSIPNPGSKETFNLLYYEADDSATKTPNNMENP 135  
 QY 121 WYVYDTIAADESFQYDIDGRVAKINTEVRSFGVRSFGYLAFODYGGCMSLIAVRVF 180  
 DB 136 WYVYDTIAADESFQYDIDGRVAKINTEVRSFGVRSFGYLAFODYGGCMSLIAVRVF 195  
 QY 181 RCPRIIONCAIFOETISGAESTSLVAARSGCIANAEDVDPIKLYCNGDEGLVPIGRG 240  
 DB 196 RCPRIIONCAIFOETISGAESTSLVAARSGCIANAEDVDPIKLYCNGDEGLVPIGRG 255

QY 241 MCKAGFEAVENGTCRGGSGTFRKANOGDEACTHCPIINSRTTSGATNCYCRRNGYRADL 300  
 DB 256 MCRPEYEVANGTCRGGSGTFRKANOGDEACTHCPIINSRTTSGATNCYCRRNGYRADL 315  
 QY 301 DPLDPCCTTIPSAQAVASSVNETSLMDEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 360  
 DB 316 DPLDPCCTTIPSAQAVASSVNETSLMDEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 375  
 QY 361 CGDNVQVAPROLGLTEPRITYSDLIARQYTFEIQAVNGYDQSPSPQFASVNTTNOA 420  
 DB 376 CGDNVQVAPROLGLTEPRITYSDLIARQYTFEIQAVNGYDQSPSPQFASVNTTNOA 435  
 QY 421 APSAIVIMHOVSRFVDSITLMSOPDPQNGYILDYELQYKEKSEYNATAIKSPNTVT 480  
 DB 436 APSAIVIMHOVSRFVDSITLMSOPDPQNGYILDYELQYKEKSEYNATAIKSPNTVT 495  
 QY 481 --GLKAGAIYFOVARTVAGYGRYSGRMFQMTAEAYQTSIOEKLPLIGSSAGLVE 538  
 DB 496 VQNLKAGITTYFOVARTVAGYGRYSGRMFQMTAEAYQTSIOEKLPLIGSSAGLVE 555  
 QY 539 LIAVYVIAIVCNRRGEERADSEYTDKLOHTSGHTPGMKITIIDPTEYEDPNEAVREFAK 598  
 DB 556 LIAVYVIAIVCNRRGEERADSEYTDKLOHTSGHTPGMKITIIDPTEYEDPNEAVREFAK 615  
 QY 559 EIDISCVKIEQYTGAGEFGEVCSGHLKLGKREIFVAIKTLKSGYTEKQORDPLSEASIM 658  
 DB 616 EIDISCVKIEQYTGAGEFGEVCSGHLKLGKREIFVAIKTLKSGYTEKQORDPLSEASIM 675  
 QY 659 GGFDPHNVIIHEGVVTKSTPVMTITEPMENGSLSDFLQNDQGFIVIOVGMKGIAAGM 718  
 DB 676 GGFDPHNVIIHEGVVTKSTPVMTITEPMENGSLSDFLQNDQGFIVIOVGMKGIAAGM 735  
 QY 719 KYLAAMNVYHRDLAFLNLTIVNSNLCKVSDGSLFLEDDTSDPYTTSALGKPIRMTA 778  
 DB 736 KYLAAMNVYHRDLAFLNLTIVNSNLCKVSDGSLFLEDDTSDPYTTSALGKPIRMTA 795  
 QY 779 PEAIQYRKFTSADSVKSYGIWMEVMSYGERPYMDTNOYINALEODYRLPPMDCSA 838  
 DB 796 PEAIQYRKFTSADSVKSYGIWMEVMSYGERPYMDTNOYINALEODYRLPPMDCSA 855  
 QY 839 LHQMLDCQKDRNHPRFGQIVNTLDMKIRPNLSLKAAAPLSSGINPLDRTIPDVT 898  
 DB 856 LHQMLDCQKDRNHPRFGQIVNTLDMKIRPNLSLKAAAPLSSGINPLDRTIPDVT 915  
 QY 899 ENTVEWEMLEATMGQYKESFANAGTSPDYVSQMMEDILRQVYLAGHOKKIINSIQVM 958  
 DB 916 ENTVEWEMLEATMGQYKESFANAGTSPDYVSQMMEDILRQVYLAGHOKKIINSIQVM 975  
 QY 959 RAQMNQIOSVEV 970  
 DB 976 RAQMNQIOSVEV 987

RESULT 5  
 EEBL\_RAT STANDARD; PRT; 984 AA.  
 ID EEBL\_RAT  
 AC P09759;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EPH-2) (ELK).  
 GN EPHB1 OR EPH2 OR ELK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTAR; TISSUE=Brain;  
 RX MEDLINE=91203869; PubMed=2017163;  
 Lhotak V., Greer P., Letwin K., Pawson T.;

[illegible]

DB 854 HOLMDCQKDNRSRFRREIVNTLDMKMRNPASLKTATVTAIVASQPLDPSIDPFTAF 913  
OY 900 NTVDWELAIKMGQYKESFANAGFTSPDYVSCMMEDIRVAVTAGHOKKLTNSIQMR 959  
DB 914 TVYDWLSAIKRVYRDSFLTAGFTSLQVMTQMSDELLRIGVLAGHOKKLTLSHSNR 973  
OY 960 AQMNQOSV 968  
DB 974 VQMNQSPV 982  
RESULT 6  
EPH1\_HUMAN STANDARD: PRT: 984 AA.  
ID EPH1\_HUMAN P54762; 043569; 095142; 095143;  
AC P54762; 043569; 095142; 095143;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE EPHRIN TYPE-B RECEPTOR 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
KINASE RECEPTOR EPH-2) (NET) (HEK6) (ELK).  
GN EPH1 OR EPH2 OR NET.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM EPH1A).  
RC TISSUE=Fetal brain;  
RX MEDLINE=96115594; PubMed=8666391;  
RA Tang X.X., Biegel J.A., Nycum L.M., Yoshioka A., Brodeur G.M.,  
RA Pleasure D.E., Ikegaki N.;  
RT "DNA cloning, molecular characterization, and chromosomal  
localization of NET(EPH2), a human EPH-related receptor protein-  
tyrosine kinase gene preferentially expressed in brain.";  
RT Genomics 29:426-437(1995).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS EPH1A TO EPH1D).  
RC TISSUE=Kidney;  
RA Stein E., Schoecklmann H.O., Daniel T.O.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP INTERACTIONS WITH GRB2 AND GRB10.  
RX MEDLINE=96394464; PubMed=8798570;  
RA Stein E., Cerretti D.P., Daniel T.O.;  
RT "Ligand activation of ELK receptor tyrosine kinase promotes its  
association with Grb10 and Grb2 in vascular endothelial cells.";  
RL J. Biol. Chem. 271:23568-23593(1996).  
CC - FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO  
EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS  
IN THE NERVOUS SYSTEM.  
CC - CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +  
PROTEIN TYROSINE PHOSPHATE.  
CC - SUBUNIT: THE LIGAND-ACTIVATED FORM INTERACTS WITH GRB2, GRB10 AND  
NCK THROUGH THEIR RESPECTIVE SH2 DOMAINS. THE GRB10 SH2 DOMAIN  
BINDS EPH1 THROUGH TYR-928, WHILE GRB2 BINDS RESIDUES WITHIN THE  
CATALYTIC DOMAIN. THE NCK SH2 DOMAIN BINDS EPH1 THROUGH TYR-594.  
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC - ALTERNATIVE PRODUCTS: 4 ISOFORMS, EPH1A (SHOWN HERE), EPH1B,  
EPH1C AND EPH1D; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC - TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN BRAIN.  
CC - SIMILARITY: CONTAINS 1 SAM DOMAIN.  
CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
RECEPTOR SUBFAMILY.  
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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: L40636; AAB08520.1; -  
DR EMBL: AF037331; AAD02030.1; -  
DR EMBL: AF037332; AAD02031.1; -  
DR EMBL: AF037333; AAB94627.1; -  
DR EMBL: AF037334; AAB94628.1; -  
DR HSP: P00523; 2PTK.  
DR MIM: 600600; -  
DR InterPro: IPR000561; -  
DR InterPro: IPR000719; -  
DR InterPro: IPR001090; -  
DR InterPro: IPR001245; -  
DR InterPro: IPR001426; -  
DR InterPro: IPR001660; -  
DR InterPro: IPR001777; -  
DR Pfam: PF01404; EPH\_1b1.1.  
DR Pfam: PF00536; SAM; 1.  
DR Pfam: PF00041; fn3; 2.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00014; FNTYPEIII.  
DR PRINTS: PR00109; TYRKINASE.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN; 1.  
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
KW Alternative splicing.  
FT SIGNAL 1 17  
FT CHAIN 1 984  
FT DOMAIN 18 540  
FT TRANSMEM 541 563  
FT DOMAIN 564 964  
FT DOMAIN 183 319  
FT DOMAIN 320 429  
FT DOMAIN 430 527  
FT DOMAIN 619 882  
FT DOMAIN 902 984  
FT SITE 982 984  
FT NP\_BIND 625 633  
FT BINDING 651 651  
FT ACT\_SITE 744 744  
FT MOD\_RES 594 594  
FT MOD\_RES 600 600  
FT MOD\_RES 778 778  
FT MOD\_RES 928 928  
FT CARBOHYD 334 334  
FT CARBOHYD 426 426  
FT CARBOHYD 480 480  
FT VARSPIC 1 27  
FT VARSPIC 617 984  
FT VARSPIC 642 682  
FT CONFLICT 12 12  
FT CONFLICT 87 37  
FT CONFLICT 152 132  
FT CONFLICT 185 135  
FT CONFLICT 274 274  
FT CONFLICT 336 336  
FT CONFLICT 367 367  
FT CONFLICT 485 485  
FT CONFLICT 813 813  
FT CONFLICT 819 819  
FT CONFLICT 847 847  
FT CONFLICT 973 973  
FT CONFLICT 984 AA; 109884 MW; 8044160E24E93A92 CRC64;  
SQ  
Query Match 76.2%; Score 3899.5; DB 1; Length 984;  
Best Local Similarity 73.8%; Pred. No. 1e-23;  
Matches 712; Conservative 130; Mismatches 120; Indels 3; Gaps 2;

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QY 2 LAABEETLMDSTTAAEAGMVAHPSPSGMEVSGYDENNNITRTYOVAVNESSONNMLRT 61
DB 15 VAAEETLMDTATAEAGMTANPASGMEVSGYDENINTRTYOVAVNEPNOONMLLT 74
QY 62 KIRRRGAHRIHVEKKFSRBOCSSIPSPGCKEFENLYYEADPDSATKTFPMMEPW 121
DB 75 TFINRGARHRIETKREFTYRDOSSLPNPGCKEFENLYYEADPDSATKTSAAWSEAPY 134
QY 122 VKVDITIADESEFOVDLGRWAKINTEVRSFPGVSRSGFYLAPODYGCSNLIARVEYR 181
DB 135 LKVDITIADESEFOVDLGRWAKINTEVRSFPGVSRSGFYLAPODYGCSNLIARVEYR 194
QY 182 KCPRTIIONGALFOETLSAESTSLVAAGSCITANAEEVDYPIKLYCNGDEMLVPIGRM 241
DB 195 KCPSTIVQFAFPEPTMTGAESTSLVANGTCIPNAEEVDYPIKLYCNGDEMLVPIGRM 254
QY 242 CKAGEEAVENGTVGRCGSPGTFKANOGEACTHCPINSRTSEATNCVCRNGYRADLD 301
DB 255 CKPGYEP-ENVVACKACACAGTFKASQAEHSGHCPSPSRSAEASPICTCTGTYRADFD 313
QY 302 PLDMPTTIPAPAVISSVNETSLMEPTPRDSGGRREDLVNIIKSCSGSGACTRC 361
DB 314 PPEVACTSPGSPRNVISIYNETSIILEMHPRETGRDVTYNIICKGRADRSRC 373
QY 362 GDNVQYAPROGLTEPRITYSDLLAHQYTFEIQAVNGYVDOSFQFASVNTTNOA 421
DB 374 DDNVQYAPROGLTEPRITYSDLLAHQYTFEIQAVNGYVDOSFQFASVNTTNOA 433
QY 422 PSAVSIMHQSRTVDSITLSNPODPONGVILDELOQYKEKELSEVATAIKSPNT -V 479
DB 434 PSTVPIHMQVSATRSITLSMPOEPONGIILDEIRYKEKELSEVATAIKSPNT -V 493
QY 480 TGLKAGAIYFOVARAVAGYGRSGMAYQTMTEABYQTSIOEKLPLTIGSSAAGLVFL 539
DB 494 DGLPGWAVYVOVARAVAGYGRSGMAYQTMTEABYQTSIOEKLPLTIGSSAAGLVFL 553
QY 540 IAVVAVIYVNRKGFERADSEYTDKLOHTYSGHITPGMKYITDPYFEDNEAVREAKE 599
DB 554 VSLVAISIVOSRRKAYSKAVYDCKLOHTYSGHITPGMKYITDPYFEDNEAVREAKE 613
QY 600 IDISCAVIEOVIGAGEFEGVSCGHLKPGKREIFVAIKTLKSGYTERKORDELSEASING 659
DB 614 IDVSFVIEEVIGAGEFEGVSCGHLKPGKREIFVAIKTLKAGYSEKORDELSEASING 673
QY 660 QPDHPNTHLEGVVTKSTPVMITTEEMENSLDSFLRONDGOVTYQVGMRLGIAAGMK 719
DB 674 QPDHPNTHLEGVVTKSTPVMITTEEMENSLDSFLRONDGOVTYQVGMRLGIAAGMK 733
QY 720 YLADMYVHRDLAARNILVNSNLVCKVSDGSLRPLEDDTSDPTYSALGKFPJRWTP 779
DB 734 YLAEMNVHRDLAARNILVNSNLVCKVSDGSLRPLEDDTSDPTYSALGKFPJRWTP 793
QY 780 EALQYKFTSASVMSYGVIMMEVMSYGERPYWDMTNOVINAIEDDYRLPPMDCPSAL 839
DB 794 EALAYKFTSASVMSYGVIMMEVMSYGERPYWDMTNOVINAIEDDYRLPPMDCPSAL 853
QY 840 HOLMLCQOKDRHRRPKFGQIYNTLDKMBRNPNNSKAMAPLSSGINTLPLDDTIDYYSF 899
DB 854 HOLMLCQOKDRHRRPKFGQIYNTLDKMBRNPNNSKAMAPLSSGINTLPLDDTIDYYSF 913
QY 900 NVVDENLEAIKMGQYKESFANAGFTSFVDVSSOMMEDILRVGVTLAGHOKKLINSIQWR 959
DB 914 TTVDDMLSAIKMQRYSFLTAGFTSLQVTVMTSDDLRLGITLAGHOKKLINSIQWR 973
QY 960 AQMNQ 964
DB 974 VOISQ 978

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AC 091571;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1A PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR XEK).
GN XEK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95215070; PubMed=7700636;
RA Jones T.L., Katayama T., Maeno M., Ong R.C., Kung H.-F., Daar I.O.;
RT "Expression of an amphibian homolog of the Eph family of receptor
RT tyrosine kinases is developmentally regulated."
RL Oncogene 10:1111-1117(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A
CC -1- ROLE IN THE DEVELOPMENT OR FUNCTION OF THE CENTRAL NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID
CC BLASTULA TRANSITION AND REAPPEARS AT LATE NEURULATION. EXPRESSED
CC AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC
CC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBQUITOUSLY
CC EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION IN
CC THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE
CC RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC -----
DR EMBL: U14164; AA074888.1; -
DR HSSP: P00523; 2PTK.
DR InterPro: IPR000719; -
DR InterPro: IPR001090; -
DR InterPro: IPR001245; -
DR InterPro: IPR001426; -
DR InterPro: IPR001660; -
DR InterPro: IPR001777; -
DR InterPro: IPR001899; -
DR Pfam: PF001404; EPH_1bd. 1.
DR Pfam: PF00536; SAM. 1.
DR Pfam: PF00041; fn3. 2.
DR Pfam: PF00069; pkinase. 1.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR. 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM. 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1. FALSE_NEG.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2. 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN. 1.
KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 985
FT DOMAIN 20 342
FT TRANSMEM 543 563
FT DOMAIN 564 985
FT DOMAIN 185 321
FT DOMAIN 322 431
FT EPHRIN TYPE-B RECEPTOR 1A.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT CYS-RICH.
FT FIBRONECTIN TYPE-III.

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FT DOMAIN 432 529 FIBRONECTIN TYPE-III.
FT DOMAIN 620 883 PROTEIN KINASE.
FT DOMAIN 910 985 SAM.
FT SITE 983 985 PDZ-BINDING MOTIF (POTENTIAL).
FT NP_BIND 626 634 ATP (BY SIMILARITY).
FT BINDING 652 652 ATP (BY SIMILARITY).
FT ACT_SITE 745 745 BY SIMILARITY.
FT MOD_RES 595 595 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 601 601 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 929 929 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 482 482 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 985 AA; 110104 MW; B672CDBF51E623 CRC64;

Query Match 73.4%; Score 3754; DB 1; Length 985;
Best Local Similarity 71.6%; Pred. No. 1e-224;
Matches 693; Conservative 131; Mismatches 134; Indels 10; Gaps 5;

OY 2 LAAVEETLMDSTTATAEIGMMVHPSPGMEVSGYDENMTITRTYOVCNVESSQNNMLRT 61
DB 17 VQAVEETLMDSTTATAEIGMMVHPSPGMEVSGYDENMTITRTYOVCNVESSQNNMLRT 76
OY 62 KETRRGARHRIHVEKESVYRDCSSIPVSGCKETPNLYYADSDATKTTPNMENPM 121
DB 77 TETRRGARHRIHVEKESVYRDCSSIPVSGCKETPNLYYADSDATKTTPNMENPM 136
OY 122 VAVDTTAADESSQNDLGRWVKINTEVRSFGVSRSGFYLAFOYDGGCMSLAVREYR 181
DB 137 LKVDTTAADESSQNDLGRWVKINTEVRSFGVSRSGFYLAFOYDGGCMSLAVREYR 196
OY 182 KCPRIITONGAIFQETLGAESTSLVAARSGCIANAEEVDPTIKLYCNGDEMLVPIGRM 241
DB 197 EMSVQONLLVPEMTGTAGESTSLVARGCIPNAEEVDPTIKLYCNGDEMLVPIGRM 256
OY 242 CRAFEAVENGIVYKCGPCSGTFRANGDCACTHCPINSTTSBGANCCVCRNGYRADSD 301
DB 257 CRAFEAVENGIVYKCGPCSGTFRANGDCACTHCPINSTTSBGANCCVCRNGYRADSD 315
OY 302 PLMPCTTIPSAFOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSGSGRGACTRC 361
DB 316 TPAPACTSVPSGRNVISYINERAILLEHMPRETGGRDVDYNIYCKCRADBRACSRG 375
OY 362 GDNVQYARQGLTEPRITYSIDLATHTQTFEIOAVNGVTDOSPEPQASVNTTNOAA 421
DB 376 DNVNVEPRQGLTEPRITYSIDLATHTQTFEIOAVNGVTDOSPEPQASVNTTNOAA 435
OY 422 PSASVIMHQVSRVDSITLSMSQPDOPNGVILDELOYEYKELSEFNATAIKSPNTV-- 479
DB 436 PSSVPIHQQVATKMSITLTSWPOEOPNGVILDELOYEYKELSEFNATAIKSPNTV-- 495
OY 480 TGLKAGAIYF---OVARFVAGYGRYSGKMFQMTAEYQTSIOEKLPLTIGSSAAGL 536
DB 496 TG---GVMWFMFSQYVARFVAGYGRYSGKMFQMTAEYQTSIOEKLPLTIGSSAAGL 551
OY 537 VFLIAVVAIVCNRRKGFEPADSEYTDKLOHTYSGHTTPMKYIYDPEYEDNEAVREF 596
DB 552 VFLIAVVAIVCNRRKGFEPADSEYTDKLOHTYSGHTTPMKYIYDPEYEDNEAVREF 611
OY 597 AKEDISCVCIEQYIGAGEGEGVSGHLKLPGRKEIFVAIKTKLKSQYTERKORDFLSEAS 656
DB 612 AKEDISCVCIEQYIGAGEGEGVSGHLKLPGRKEIFVAIKTKLKSQYTERKORDFLSEAS 671
OY 657 IMGFDPHNVYHLEGVYTKSTPVMTTEPMENGLSDFLRQNGQFVIVLYVGMKSLIA 716
DB 672 IMGFDPHNVYHLEGVYTKSTPVMTTEPMENGLSDFLRQNGQFVIVLYVGMKSLIA 731
OY 717 GAKTLADNMYHRLAARNTLVNSLVCKVSDGLSRLDDPTSDPTYSALGKGFIRW 776
DB 732 GAKTLADNMYHRLAARNTLVNSLVCKVSDGLSRLDDPTSDPTYSALGKGFIRW 791

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OY 777 TAPDAIYKREFTASDVWSYGIYMMEMVSGEERYWDMTNOVDYINAEODYRLPMPDCP 836
DB 792 TAOEALAYRREFTASDVWSYGIYMMEMVSGEERYWDMTNOVDYINAEODYRLPMPDCP 851
OY 837 SALHQLMDCQMDQNRNIRPEFGQIVNTLDMKIRNPNSLKAAPLSSGINLPLDRTIPDY 896
DB 852 ALHQLMDCQMDQNRNIRPEFGQIVNTLDMKIRNPNSLKAAPLSSGINLPLDRTIPDY 911
OY 897 TSEPTVDEMLEAIRKMGYKESFANAGTSPDVYSQAMMEIILAVGTIAGHOKKIINSIO 956
DB 912 SAFTSVDMVDSAIKMGYKESFANAGTSPDVYSQAMMEIILAVGTIAGHOKKIINSIO 971
OY 957 VMRAQNNQ 964
DB 972 SMRVQITQ 979

RESULT 8
EPBL_CHICK
ID EPBL_CHICK STANDARD; PRT; 984 AA.
AC Q07494;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 1 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
DE RECEPTOR EPH-2) (TYROSINE KINASE CER6 RECEPTOR) (FRAGMENT).
CN EPHB1 OR CER6.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=93286394; PubMed=8510926;
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO
CC EPHRIN-B1, -B2 AND -B3. MAY BE INVOLVED IN CELL-CELL INTERACTIONS
CC IN THE NERVOUS SYSTEM.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE 10-DAY EMBRYO,
CC AND IN ADULT BRAIN, LUNG, HEART AND SKELETAL MUSCLE. LOW LEVELS OF
CC EXPRESSION DETECTED IN ALL OTHER ADULT TISSUES TESTED.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC -----
CC EMBL: 219110; GAA79536.1; -
CC HSSP: P00523; 2PRT.
CC InterPro: IPR000561; -
CC InterPro: IPR000719; -
CC InterPro: IPR001090; -
CC InterPro: IPR001245; -
CC InterPro: IPR001426; -
CC InterPro: IPR001600; -
CC InterPro: IPR001777; -
CC Pfam: PF01404; Eph_1hd; 1.
CC Pfam: PF00536; SAM; 1.

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DR pfam: PF00041; fn3; 2.  
 DR PROSITE: PS00107; KINASE\_1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR\_1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM\_1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; PARTIAL.  
 DR PROSITE: PS01861; EGF\_2; UNKNOWN\_1.  
 DR TRANSFERASE: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Repeat.  
 FT DOMAIN 1 541 EXTRACELLULAR (POTENTIAL).  
 FT TRAMEM 542 562 POTENTIAL.  
 FT DOMAIN 563 584 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 164 300 CYS-RICH.  
 FT DOMAIN 301 410 FIBRONECTIN TYPE-III.  
 FT DOMAIN 411 527 FIBRONECTIN TYPE-III.  
 FT DOMAIN 619 882 PROTEIN KINASE.  
 FT SITE 909 984 SAM.  
 FT SITE 982 984 PDZ-BINDING MOTIF (POTENTIAL).  
 FT NP\_BIND 625 633 ATP (BY SIMILARITY).  
 FT BINDING 651 651 ATP (BY SIMILARITY).  
 FT ACT\_SITE 744 744 BY SIMILARITY.  
 FT MOD\_RES 594 594 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 600 600 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 778 778 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 928 928 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 SQ SEQUENCE 984 AA; 109519 MW; EF06C83B63A13A1 CRC64;

Query Match 72.4%; Score 3704; DB 1; Length 984;  
 Best Local Similarity 70.2%; Pred. No. 1,3e-221;  
 Matches 687; Conservative 120; Mismatches 150; Indels 22; Gaps 3;

QY 7 ETLNDSTTATATLAWVPPSGEVEGSDENMTITRYOVGVNESSQNMNLTKEIRR 66  
 DB 1 ETLNDSTTATATLAWVPPSGEVEGSDENMTITRYOVGVNESSQNMNLTKEIRR 60  
 QY 67 RGARHIVHEKFSYRDCSSIPSYVGSGKEFNLYYADDSATKTFPNMKNPVKVD 126  
 DB 61 RGARHIVHEKFSYRDCSSIPSYVGSGKEFNLYYADDSATKTFPNMKNPVKVD 120  
 QY 127 IADSEFSQVLDGGRVKNITEVRSFGVRSFYLAFOYGGCMSLIAVRYRCPR 186  
 DB 121 IADSEFSQVLDGGRVKNITEVRSFGVRSFYLAFOYGGCMSLIAVRYRCPR 180  
 QY 187 IONGAIFQELSGAESSTLVAAAGSCIANAEVDVPIKLYCNGDGEVLVIGRCMKAGF 246  
 DB 181 VONFAIRPETMTAGESTSLVTAGTCTIPNAEVDVPIKLYCNGDGEVLVIGRCMKAGF 240  
 QY 247 EAVENGTVRGCGSTGFKNQGDGACHTCPINSRTSEGATNCVANGYRRADLDLMP 306  
 DB 241 EP-BNNVACACACAGTFFKASQAGLACRCPNRSASAEPLCACRNGFRADLDLPTAA 299  
 QY 307 CTTIPSPAVAVISVNETSLMELETPPRDSGREDLVNIIKSCSGSGRACRCDNYQ 366  
 DB 300 CTVSPGSPRVAVISVNETSLMELETPPRDSGREDLVNIIKSCSGSGRACRCDNYQ 359  
 QY 367 YABROGLTEPRYISDLDLAHYEIQAVNGVTOQSFQFASVNTTQAAPSAVS 426  
 DB 360 FVPRQGLTEPRYISDLDLAHYEIQAVNGVTOQSFQFASVNTTQAAPSAVS 419  
 QY 427 IMHGVSRVDSITLWSQPDQNGVITLDELQYERK-----ELSEY 467  
 DB 420 IMHGVSRVDSITLWSQPDQNGVITLDELQYERK-----ELSEY 479  
 QY 468 NATATSPNT--VTGLKAGATVYOVRAVYAGRGSGKGFOTMBAEQVSIQEK 525  
 DB 480 NSSVAVSQTNTARLEGRLRGAMVYVQVRAVYAGRGSGKGFOTLDDDDKSELRL 539  
 QY 526 PLTIGSSAAGLVLAIVVAVIACNRKGFERADSEYTKLQHYTSGHITPGMKIYIDFT 585  
 DB 540 PLTIGSSAAGLVLAIVVAVIACNRKGFERADSEYTKLQHYTSGHITPGMKIYIDFT 599

QY 586 YEDNEAVREFAKEIDISCKIEQVIGAGFEFGVSGHKLTPKREIFVAKTLKSGYTE 645  
 DB 600 YEDNEAVREFAKEIDISCKIEQVIGAGFEFGVSGHKLTPKREIFVAKTLKSGYTE 659  
 QY 646 KORRDFEASESINGQFHPVHLEGVYKSTPVMTITTEMENGSLDSFLRNDGQFTYI 705  
 DB 660 KORRDFEASESINGQFHPVHLEGVYKSTPVMTITTEMENGSLDSFLRNDGQFTYI 719  
 QY 706 QLVGMRLGIAAGMKYTLADNMYVARDLAARNILVNSLVKVSDFGSLREDTSDPTT 765  
 DB 720 QLVGMRLGIAAGMKYTLADNMYVARDLAARNILVNSLVKVSDFGSLREDTSDPTT 779  
 QY 766 SALGKRPIMTAPALQVRKFTSASDVWSYGIYMAEVSYSGERPYMDTNDVINAIEQ 825  
 DB 780 SALGKRPIMTAPALQVRKFTSASDVWSYGIYMAEVSYSGERPYMDTNDVINAIEQ 839  
 QY 826 DYRLPPMDCPSALHQLMIDCMQKDRNRRFGQIYNTLDKMIKPNNSLKAAAPLSSGIN 885  
 DB 840 DYRLPPMDCPSALHQLMIDCMQKDRNRRFGQIYNTLDKMIKPNNSLKAAAPLSSGIN 899  
 QY 886 LPLDRTIDYTSFNTVDEMLAIKMGQYKESFPANAGFTSPDVSQMMEDILRYGVTLA 945  
 DB 900 QPLDRTIDYTSFNTVDEMLAIKMGQYKESFPANAGFTSPDVSQMMEDILRYGVTLA 959  
 QY 946 GHQKTIINSIQVRAQMO 964  
 DB 960 GHQKTIINSIQVRAQMO 978

RESULT 9  
 EPR3\_CHICK  
 ID EPR3\_CHICK STANDARD; PRG: 988 AA.  
 AC 007498;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 3 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE  
 RECEPTOR CEK10) (FRAGMENT).  
 GN EPHB3 OR CEK10.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 ON NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93288394; PubMed=8510926;  
 RA Sajjad F.G., Pasquale E.B.;  
 RT "Five novel avian Eph-related tyrosine kinases are differentially  
 expressed.";  
 RL Oncogene 8:1807-1813(1993).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM: MAY BE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN 10-DAY EMBRYONIC BRAIN AND BODY  
 CC TISSUES. PROMINENT EXPRESSION IN KIDNEY. LOWER EXPRESSION IN LUNG,  
 CC AND BARELY DETECTABLE IN BRAIN, LIVER, HEART, SKELETAL MUSCLE AND  
 CC THYMUS.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: BEYONDS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BEYONDS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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CC EMBL, Z19061; CAA79511.1; -

DR HSSP; P00523; 2PTK.

DR InterPro; IPR000179; -

DR InterPro; IPR001090; -

DR InterPro; IPR001245; -

DR InterPro; IPR001426; -

DR InterPro; IPR001660; -

DR InterPro; IPR001777; -

DR Pfam; PF00041; In3; 2.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00536; SAM; 1.

DR Pfam; PF01404; EPH\_1bd; 1.

DR PRINTS; PR00014; FNTYPELIT.

DR PRINTS; PR00109; TYRKINASE.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.

DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.

DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Alternative splicing; Repeat.

KW NON\_TER

FT DOMAIN <1 534

FT TRANSMEM 535 585

FT DOMAIN 556 988

FT DOMAIN 171 308

FT DOMAIN 309 421

FT DOMAIN 422 520

FT DOMAIN 623 886

FT DOMAIN 913 988

FT SITE 986 988

FT NP\_BIND 629 637

FT DISULFID 53 88

FT BINDING 655 655

FT ACT\_SITE 748 748

FT MOD\_RES 598 598

FT MOD\_RES 604 604

FT MOD\_RES 782 782

FT MOD\_RES 932 932

FT CARBOHYD 323 323

FT CARBOHYD 418 418

FT VARSPPLIC 558 572

SEQ SEQUENCE 988 AA: 109578 MW: EER0D39C03FFD3C8 CAC64:

Query Match 71.3%; Score 3649.5; DB 1; Length 988;

Best Local Similarity 70.0%; Pred. No. 3e-218;

Matches 683; Conservative 120; Mismatches 144; Indels 29; Gaps 6;

QY 16 TAEIGMNVHPSPGMEVSGYDENMNTIRTYOVNVESSNNMLRKRFRRCAGRIHVE 75

DB 21 TSELAMTTHETGEEVSGYDEAMNPRTIROYCNVREANNNMLRKRFRIR0DOV0YVE 80

QY 76 MKSIVRCSSIPSPGSCKEFTPNLYYEADFSATKTFPMNENPMVKYDTIADSEFSQ 135

DB 81 LKFTVRCSNIPNIPGSKETFNLYTESPTDSANSPPMNPYIKVDIAPDESFSK 140

QY 136 VDLGGRVAKINTEVRSFSPVSRSGFYLAPODYGGCMLIAVAVRYRKRCPRIIONGAIPOE 195

DB 141 LDES---RVNTKVRSGPLSKNGFYLAQDLGACMLISVRAFYKKCSNTIAGFAIFPE 196

QY 196 TLSGAESTSLVANGSCIANAEVDVIRIKYCNQDGMVLVPIGRCKMAKAEVAVENTVC 255

DB 197 TLTAETFTSLVAVGTCTIPANAVEVSPKLKLYCNDGEMVAVGACCTCAAGIEPAMKDTQC 256

QY 256 RGCSSGTFKNGDEACTHCPINSRTSSEGAFTNCVCRNGYRADIPLDMPCTTISAPQ 315

DB 257 QACPGPFTKSKQGGPCSPCPPNRRTTAGAATYVICSGGFRADADADACISVPEAPR 316

QY 316 AVISSVNETSLIMLEWTPPRDPSGGRDLVYNICKSCSGSGGACTRCGDNVYAPROL--- 372

DB 317 SVLSNNEISLVLEMSIPDAGCRDDLIVNICKKSVSRRLCSRDDNVEVPRDLGLT 376

QY 373 GLTEPRITISDLAHTQYTFEEIOAVNGVTDQSPSPQFASVNTTNOAPASVNTIMQVS 432

DB 377 GLTERRIISKVNAHPYTFEEIOAVNGVSSISKSPPHFAVNTTNOAPASVNTIMHLS 436

QY 433 RTVDSITLSWOPDPPGVLDELQYERE-LSEYNATAIKSPNTV--TGIKAGAIYV 489

DB 437 STGSMWLSWTPPERPGLILDELKIKSEKOGGDDIANTVISOQNSVLDGLKAAARM 496

QY 490 FOVARTVAGYGRYSGLMPQMTAEYQTSIOEKLPLIIGSSAGLVLLAVVAIYC 549

DB 497 VQVARTVAGYGRSLPTEFQTAEDGSTKTEQELPLIVGATAGILVAVVIAIYC 556

QY 550 NRGFE-----ERADSETDLQHYTSGHITPGKVIIDPTTYEDPNEAVR 594

DB 557 FRKGMVTEOLLSPGKRKNRSTDPETTERLQOY---VTPGKVIIDPTTYEDPNEAVR 612

QY 595 EFAKEIDISCVKIPQVIGAGEFEGVCSGHLKLPKREIFAIRKTLKSGYTEKORDFLSE 654

DB 613 EFAKEIDISCVKIEVIGAGEFEGVCSGRLKLGRRRIFAIRKTLKSGYTEKORDFLSE 672

QY 655 ASINGQDPNVVHLESVYTKSPVMTTEPMENGSLDSTLRONDQGFYIOLVGMIRGI 714

DB 673 ASINGQDPNVVHLESVYTKSPVMTTEPMENGSLDSTLRONDQGFYIOLVGMIRGI 732

QY 715 AAGKVIADNMVYVRDLAARIIIVNSMLVCKVSPFGLSRLEDDTSPPTYSAAGKFI 774

DB 733 AAGKVIADNMVYVRDLAARIIIVNSMLVCKVSPFGLSRLEDDTSPPTYSAAGKFI 792

QY 775 RMTAPEALQYRKETSASDVSYGIWMEVMSYGERPYWMTNDQVINAIDQYRLPPMD 834

DB 793 RMTAPEALQYRKETSASDVSYGIWMEVMSYGERPYWMTNDQVINAIDQYRLPPMD 852

QY 835 CPSPALHOLMDCKOKDRHRKPGQIYNTLDKMTIRNNSLKAMPALSSGINLPDLRTIP 894

DB 853 CPSPALHOLMDCKOKDRHRKPGQIYNTLDKMTIRNNSLKAMPALSSGINLPDLRTIP 912

QY 895 DYSFNTVDMLAETKMGQYKESFANAGFTSFDVVSQMMEDILRVGVTIAGHOKTILNS 954

DB 913 DYTFTTITGMDLDAIKMGRYKENFVAGFASFDLVAQMTADLIRIGVTIAGHOKTILNS 972

QY 955 IOVMRAQNNQIOSVEY 970

DB 973 IOVMRAQNNQIOSVEY 988

RESULT 10

EPB3\_HUMAN

ID EPB3\_HUMAN STANDARD: PRT: 998 AA.

AC P54753;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HEK-2).

GN EPHB3 OR ETK2 OR HEK2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI-Taxid=9606;

RN (11)

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=93390963; PubMed=8397371;

RA Boehme B., Holtrich U., Wolf G., Lutz H., Grzeschik K.-H., Streibhardt K., Rebsamen-Waigmann H.;

RT "PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2."

RT Oncogene 8:2857-2862(1993).

CC -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. BINDS TO EPHRIN-B1 AND -B2.

```

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X75208; CAA53021.1; -
DR HSSP; P00523; 2PTK.
DR MIM; 601839; -
DR InterPro; IPR000719; -
DR InterPro; IPR001090; -
DR InterPro; IPR001245; -
DR InterPro; IPR001426; -
DR InterPro; IPR001650; -
DR InterPro; IPR001777; -
DR Pfam; PF01404; EPH_Lbd; 1.
DR Pfam; PF00536; SAM; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00014; ENTPEPIT.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transferrase; Tyrosine-protein kinase: ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 33
FT CHAIN 34 998
FT DOMAIN 34 598 EPHRIN TYPE-B RECEPTOR 3.
FT TRANSMEM 560 580 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 581 598 POTENTIAL.
FT DOMAIN 199 336 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 337 448 CYS-RICH.
FT DOMAIN 449 544 FIBRONECTIN TYPE-III.
FT DOMAIN 633 896 FIBRONECTIN TYPE-III.
FT DOMAIN 923 988 PROTEIN KINASE.
FT SITE 996 998 SAM.
FT NP_BIND 639 998 PDZ-BINDING MOTIF (POTENTIAL).
FT BINDING 665 665 ATP (BY SIMILARITY).
FT ACT_SITE 758 758 ATP (BY SIMILARITY).
FT MOD_RES 608 608 BY SIMILARITY.
FT MOD_RES 614 614 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 792 792 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 942 942 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 998 AA; 110286 MW; 57C82C397CC61103 CRC64;

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Query Match 71.0%; Score 3632.5; DB 1; Length 998;  
 Best Local Similarity 70.5%; Pred. No. 3.5e-217;  
 Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

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QY 4 AVEETLMDSTTATLGMVHPSPGMEVSGDENMNTIRYQVCNVPRESSONMWRKRF 63
DB 37 ALEETLMOTKWTSLATNSHPESGHEVSGYDEAMNIRYQVCNVPRESSONMWRKRF 96
QY 64 IRRGAHRIHEMKFSPVDCSSIPSPGCKETFNLYYEADEFSAATKTFPMNMENPMVK 123
DB 97 IWRDVORHYVELKFTVDCNSIPNIPGCKETFNLYYEADEFSAATKTFPMNMENPMVK 156

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QY 124 VDTIADDESPQVLDGGRWAKINTEVRSFGPVSRSGFYLAFODYGCSMLAVRVYRKC 183
DB 157 VDTIADDESPQVLDGGRWAKINTEVRSFGPVSRSGFYLAFODYGCSMLAVRVYRKC 212
QY 184 PRICNGAIFQETLSGAEESTSLVAAAGSCIANAEVDVIRIKYCGNDEGMVPIRCKCK 243
DB 213 ASYTAGFALFPPELTIGAEPTSLVIAAGTICPNAVEVSPKLYCNGDEMDMPVAGACTCA 272
QY 244 AGEAEVNGSTVRCGCESTGFKANOGDEACTHPCINSRTTSEGATCVCVRNGYRDLPL 303
DB 273 TGHEPAKESQCRPCPGSYKAKOGEGPCLPCPRASRTTSPASICTHNNFYRADSDSA 332
QY 304 DMCCTIPAPQAVISSVETSLMEPTPPRSGREDLVNITCKSC--GSGRGACTRC 361
DB 333 DSACTTVPSPRGVLSNVEVSLLEWSEPRDLGVRDLLVNTICKCKHGGAGGASCSRC 392
QY 362 GDNVQYAPRQLGLTEPRYISDLAHTQYTFEIAQVNGVTSQSPSPQFASVNTTNOA 421
DB 393 DNVETVPRLGLSPRVHTSLAHTRYTEVOAVNGVSGSKPLPPRYAAVNTTNOA 452
QY 422 PSAVIMQVSTVSTLSMSQDPQNGVILDELOYEKELSEYNATAIKSPNTV-- 479
DB 453 PSEVPTLRHSSGSSSLTSLSNAPRPNPVGILDEYEMKFEK--SGIASVTSQMSVOL 510
QY 480 TGLKAGAIYFQVRYATVAGYGRVSGKMYFOTME-AEYQTSIDEKPLTIGSSAGLVF 538
DB 511 DGLRPDARTVQVRYATVAGYGRVSGKMYFOTME-AEYQTSIDEKPLTIGSSAGLVF 570
QY 539 LIAVVVIAIVCNRGFEADSEYTLQHYTSGHITPGMKIYIDPFYEDPNEVREFAK 598
DB 571 VYAAVVIAIVCNRGFEADSEYTLQHYTSGHITPGMKIYIDPFYEDPNEVREFAK 626
QY 599 EDISCVIEBOVAGGEYSCGHLKPKRELFVAIKTLKSYTERKORDTSEASIM 658
DB 627 EIDVSCVIEBOVAGGEYSCGHLKPKRELFVAIKTLKSYTERKORDTSEASIM 686
QY 659 GQDFHPVNIHLEGVATKSTPVMIITTEFMENGLDSFLRNDGQGTVQLQGMRLGIAAG 718
DB 687 GQDFHPVNIHLEGVATKSTPVMIITTEFMENGLDSFLRNDGQGTVQLQGMRLGIAAG 746
QY 719 KYLDAMNVHDLAARNLVNSNLVCKVSDPGLSRPLEDTSPPTYSALGKFRPRMTA 778
DB 747 KYLDAMNVHDLAARNLVNSNLVCKVSDPGLSRPLEDTSPPTYSALGKFRPRMTA 806
QY 779 PEATQYKFTSASDVMSYGIYMEVMSYGERPMDNODVINAIEDVRLPPMDCPSA 838
DB 807 PEATQYKFTSASDVMSYGIYMEVMSYGERPMDNODVINAIEDVRLPPMDCPSA 866
QY 839 LHOQLMDCQKDRNRHRRKFCQIVNTLDKMRNPSLKAAPLSSGINTPLDLRTIPDYS 898
DB 867 LHOQLMDCQKDRNRHRRKFCQIVNTLDKMRNPSLKAAPLSSGINTPLDLRTIPDYS 926
QY 899 FNTYDEWLEAIKMGQYSEFANAGTSPFDVYSGMMEDILRVYTLAGQKTLNSIQW 958
DB 927 FTYTGDMLEAIKMGQYSEFANAGTSPFDVYSGMMEDILRVYTLAGQKTLNSIQW 986
QY 959 RAQMNQIQSYEV 970
DB 987 RLQMNQTLPIVOV 998

```

RESULT 11  
 EPH3\_MOUSE  
 ID EPH3\_MOUSE STANDARD; PRT; 993 AA.  
 AC P54754; 062214;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN  
 KINASE RECEPTOR MOK-5) (DEVELOPMENTAL KINASE 5) (SEK-4).  
 GN EPHB OR ETK2 OR MOK5 OR SEK4.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=Embryo;  
 RX MEDLINE=96074837; PubMed=7478528;  
 RA Ciossek T., Lerch M.M., Ullrich A.;  
 RT "Cloning, characterization, and differential expression of MDK2 and  
 RT MDK5, two novel receptor tyrosine kinases of the eck/eph family.";  
 RL Oncogene 11:2085-2095(1995).  
 RN [2]  
 RP SEQUENCE OF 719-993 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE=Brain;  
 RX MEDLINE=95034306; PubMed=7947319;  
 RA Becker N., Seltanidou T., Murphy P., Mattel M.G., Topilko P.,  
 RA Nieto A., Wilkinson D.G., Charnay P., Giliardi P.;  
 RT "Several receptor tyrosine kinase genes of the Eph family are  
 RT segmentally expressed in the developing hindbrain.";  
 RL Mech. Dev. 47:3-17(1994).  
 RN [3]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20171264; PubMed=10704386;  
 RA Imondi R., Wideman C., Kaprielian Z.;  
 RT "Complementary expression of transmembrane ephrins and their receptors  
 RT in the mouse spinal cord: a possible role in constraining the  
 RT orientation of longitudinally projecting axons.";  
 RL Development 127:1397-1410(2000).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +  
 CC PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE RETINAL GANGLION  
 CC CELL LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISK.  
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Z49086; CAA88910.1; -  
 DR HSSP: P00523; 2PTR.  
 DR MGD: MGI:104770; Ephb3.  
 DR InterPro: IPR000719; -  
 DR InterPro: IPR001090; -  
 DR InterPro: IPR001245; -  
 DR InterPro: IPR001426; -  
 DR InterPro: IPR001660; -  
 DR InterPro: IPR001777; -  
 DR Pfam: PF01404; Eph\_1bd; 1.  
 DR Pfam: PF00536; SAM; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0014; TYRYPEIII.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 29  
 FT CHAIN 30 993  
 FT DOMAIN 30 554  
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 555 575 POTENTIAL.  
 FT DOMAIN 576 595 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 596 615 CYS-RICH.  
 FT DOMAIN 616 635 FIBRONECTIN TYPE-III.  
 FT DOMAIN 636 655 FIBRONECTIN TYPE-III.  
 FT DOMAIN 656 675 PROTEIN KINASE.  
 FT DOMAIN 676 695 SAM.  
 FT SITE 696 715 PDZ-BINDING MOTIF (POTENTIAL).  
 FT NE\_BIND 716 735 ATP (BY SIMILARITY).  
 FT BINDING 736 755 ATP (BY SIMILARITY).  
 FT ACT\_SITE 756 775 BY SIMILARITY.  
 FT MOD\_RES 776 795 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 796 815 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 816 835 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CARBOHYD 836 855 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CONFLICT 856 875 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CONFLICT 876 895 R -> Q (IN REF. 2).  
 SQ SEQUENCE 993 AA; 109585 MW; 0B66A4D391266C79 CRC64;

Query Match 70.4%; Score 3604; DB 1; Length 993;  
 Best Local Similarity 70.1%; Pred. No. 2e-215;  
 Matches 683; Conservative 111; Mismatches 163; Indels 18; Gaps 6;

QY 4 AVEETLMDSTTAETAEIEMVHPSPGMEVSGYDENMTITRTYVCVNFSSONNMILRTKF 63  
 DB 29 ALIETLMDTKWYSELAWTSHPSGMEVSGYDEANMIRTYOVCVNRESSONMILRTGF 88  
 QY 64 IRRGAHRIHEMKFVSRCSSIPSVSGKRETNLYYADPDSATKPFPMNENPWTK 123  
 DB 89 IMREVOHRYVELKFTVDCNSIPNIPSGKEFNLEYADSDVASSPFMENPWTK 148  
 QY 124 VDTLADESPQVGLGRWKINTEVRSFVSRSGLYAFODYGGCMLIAVREYRKC 183  
 DB 149 VDTLADESPQVGLGRWKINTEVRSFVSRSGLYAFODYGGCMLIAVREYRKC 204  
 QY 184 PRIIONAIFQELTSGAESTLVNARSGCIAMAEVDVPIKLYCNGDEMLVYIGCMCK 243  
 DB 205 ASTAGAFALFPELTGAPSTLVLAIPGTCIANAVEVSPKLKCNCGEMVPGVACTCA 264  
 QY 244 AGFEAVENGIVRCGFSSTEFKANGDEACHCPINSTSESGATNCVRCRNGYRADIDPL 303  
 DB 265 TGHEPAKESQCRACFPSPSYAKQGEGLPCPNSTSTSPASITGCHNNFRAEDSDA 324  
 QY 304 DMPCTTIPSAQAVISVNETSLMLEWTPPRDSGRDVLVNIICKSGSGRGA----C 358  
 DB 325 DSACTTESPPRGVLSNENETSLIEMSEPRDLGRODLVNYVICKRCRSGSGGPGPATC 384  
 QY 359 TRCGDNVOYAPROGLTEPRYISDLAHTQYTFEIQAVNVTQSPSPQAFANVTITN 418  
 DB 385 SRCDDNVEFVPROGLITERRVAHISHLAHTRYTEVOAVNVSQSPPLPRYAVANVTITN 444  
 QY 419 QAAPSAVSIMHOVSRTYVITLSMSQDOPQGVILDELYQYKELESEYNATAKSPNT 478  
 DB 445 QAAPSEVPTLHSSGSSLSLSNAPPRPANGVILDELYQYKELESEYNATAKSPNT 502  
 QY 479 V--TSLKAGATVFOVRRATVAGYGRYSGKMYFOTMB-AEYQTSIQEKLPLIIGSSAAG 535  
 DB 503 YOLDGLDPARVVOVRRATVAGYGRYSGKMYFOTMB-AEYQTSIQEKLPLIIGSSAAG 562  
 QY 536 LVFLAVVAVIAVCKRQPERADSEYTDKLOHYTSGHTTPMKIYIDPFYEDNEAVRE 595  
 DB 563 FVFMVAVVAVIAVCKRQPERADSEYTDKLOHYTSGHTTPMKIYIDPFYEDNEAVRE 618  
 QY 596 FAKEDIDSCVTEQYVAGEFEVSGHLKLGKREIFAIRKTLKSGYTEKORDPFLSEA 655  
 DB 619 FAKEDIDSCVTEQYVAGEFEVSGHLKLGKREIFAIRKTLKSGYTEKORDPFLSEA 678  
 QY 656 SIMGQDFHPNVTHLRVYTKSPVYITTEPMNGSLDSEFLNONGQFVIVDVGMLRGIA 715  
 DB 679 SIMGQDFHPNVTHLRVYTKSPVYITTEPMNGSLDSEFLNONGQFVIVDVGMLRGIA 738

QY 716 AGKYLADNNVYHRLAARNILVNSLVCKVSDGLSRLEDDTSDPTYSALGKFPFR 775  
 DB 739 AGKYLSENNVYHRLAARNILVNSLVCKVSDGLSRLEDDTSDPTYSALGKFPFR 798  
 QY 776 WTAPALVYRFTSADSVWGVWMEVMSYGERPYNMTNODYNAIEODYRLPMDPC 835  
 DB 799 WTAPALVYRFTSADSVWGVWMEVMSYGERPYNMTNODYNAIEODYRLPMDPC 858  
 QY 836 PSLALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPSLAKMAPLSGGINPLDRTIPD 895  
 DB 839 PSLALHQLMLDCWQKDRNHRPKFGQIVNTLDKMRNPSLAKMAPLSGGINPLDRTIPD 918  
 QY 896 YTSFTVDMENLEATKMGKYSFNAAGTSPDVYSQMMEDILRVGYTLACHQKILNISI 955  
 DB 919 YTSFTVDMENLEATKMGKYSFNAAGTSPDVYSQMMEDILRVGYTLACHQKILNISI 978  
 QY 956 QVRAQNMNQIOSVEY 970  
 DB 979 QDMRLQNMNQTLPPGV 993

## RESULT 12

EPBB\_XENLA STANDARD; PRT; 902 AA.

AC Q91736;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE EPHRIN TYPE-B RECEPTOR 1B (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE

DE RECEPTOR XELK) (FRAGMENT).

GN XELK.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI\_TaxID=8335;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96068901; Pubmed=7478602;

RT Scales J.B., Manning R.S., Renaud C.S., Shea L.J., Sargent T.D.;

RT "Novel members of the eph receptor tyrosine kinase subfamily expressed

RL Oncogene 11:1745-1752(1995)."

CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY

CC SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN

CC TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN THE BRAIN AND

CC SPINAL CORD AND IN THE FIRST AND FOURTH VISCERAL ARCHES. MOST

CC ABUNDANT IN ADULT BRAIN, WITH LOWER LEVELS IN EYE, HEART, OVARY,

CC OVIDUCT, LUNG AND PHARYNX.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.

CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

CC -----

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

CC EMBL: L43621; AAA93527.1; -

DR HSSP: P00523; 2PTR.

DR InterPro: IPR000719; -

DR InterPro: IPR001090; -

DR InterPro: IPR001245; -

DR InterPro: IPR001426; -

DR InterPro: IPR001660; -

DR InterPro: IPR001777; -

DR Pfam: PF01404; Eph\_1bd; 1.  
 DR Pfam: PF00336; SAM; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; pk\_nase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN; 1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Repeat.  
 FT NON\_TER 1  
 FT DOMAIN 1  
 FT TRANSMEM 460  
 FT DOMAIN 461  
 FT DOMAIN 481  
 FT DOMAIN 101  
 FT DOMAIN 238  
 FT DOMAIN 348  
 FT DOMAIN 537  
 FT DOMAIN 827  
 FT SITE 902  
 FT NP\_BIND 902  
 FT BINDING 543  
 FT ACT\_SITE 569  
 FT MOD\_RES 512  
 FT MOD\_RES 518  
 FT MOD\_RES 696  
 FT MOD\_RES 846  
 FT CARBOHYD 252  
 FT CARBOHYD 344  
 FT CARBOHYD 398  
 FT SEQUENCE 902 AA; 100850 MW; CCB9ABF7D39273CA CRC64;

Query Match 70.2%; Score 3593.5; DB 1; Length 902;  
 Best Local Similarity 73.1%; Pred. No. 7.8e-215;  
 Matches 657; Conservative 125; Mismatches 110; Indels 7; Gaps 4;

QY 70 HRIHEKFSYRDCSSIPSVGSKETPNLYYRAD--FSSATTFEPNMMENPVAVDTI 127  
 DB 1 HRVYEAKFTYRDCSSLPNVPFGSKETPNLYYETDSDNINIKSTF--WNESPYLKVDTI 58  
 QY 128 AADSFQVDLGNVNMINEVRSFGVSRSGEFLAQDYGCGMSLAVAVFYRKCPRII 187  
 DB 59 AADSFQVDLGNVNMINEVRSFGVSRSGEFLAQDYGCGMSLAVAVFYRKCPRII 118  
 QY 188 ONGALPQETLSGAEASTLVARGSCINAAEVDVPIKLYNGDGEWLVPTRCKRAGE 247  
 DB 119 ONFAVFEETKGAESTLVARGSCINAAEVDVPIKLYNGDGEWLVPTRCKRAGE 178  
 QY 248 AVENGVCRCGPGSTGFRKANGDEACTHCPINSRTSGATNGVCRNGYVRADLDPMDC 307  
 DB 179 P-ENHVVCKACPAKMFANANGMGICACQNPANSRSTSEASITCIRNGYVRADLDPEAC 237  
 QY 308 TTITSAQAVIYSSVNEISLMEVTPPDGSGREDLVYNTICKSCGSGRACRNGDVOY 367  
 DB 238 TTVSGSRNVIYVNEISLMEVTPPDGSGREDLVYNTICKSCGSGRACRNGDVOY 297  
 QY 368 APRQLGTEPRYISDLAHTOYTFELIANGVTDOGPSPOGASVNTITNOAAPSVAI 427  
 DB 298 VPRQLGTEPRYISDLAHTOYTFELIANGVTDOGPSPOGASVNTITNOAAPSVAI 357  
 QY 428 MHOVSRTVDSITLSWSPQDQPCVILDEYQYKELSEYNATIAKSPNT--VTGLKAG 485  
 DB 358 MHOVKATKMSITLSWSPQDQPCVILDEYQYKELSEYNATIAKSPNT--VTGLKAG 417  
 QY 486 AIYVQVARTVAGYRGYSGKMYFORMTEAEYQTSQELPLITSSAAGVFLAAVVI 545  
 DB 418 VYVVOVARTVAGYRGYSGKMYFORMTEAEYQTSQELPLITSSAAGVFLAAVVI 477  
 QY 546 AIVCNRRGERADSEYTDLQHYTSGHITPGMKIYIDPTTYDPEAVREFAKEIDISCV 605

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DB 478 SIVSRRKRTYSKEAVYSDKLQHYSTGRGSPGMKIYIDPTEYEDNEAVREFAKEIDVSVF 537
QY 606 KIEOYIGAGEGECVSSGLTKLPGKREIFVALIKTLKSGYTEKORDFSEASIMGOFDPHN 665
DB 538 KIEEYIGAGEGECVSSGLTKLPGKREISVALIKTLKAGISEORDFSEASIMGOFDPHN 597
QY 666 VTHLEGVYTKSTPVMILTEFEMENGSLDFLRONDQOFTVIOVLGRLGIAAGMYLADMN 725
DB 598 IRLLEGVYTKSPVMILTEFEMENGSLDFLRONDQOFTVIOVLGRLGIAAGMYLADMN 657
QY 726 VYHRLAARNILVNSNLVCKVSDPGLSFLDDSDPTTYSALGKFPRIKRTAEALQYR 785
DB 658 YVHRLAARNILVNSNLVCKVSDPGLSFLDDSDPTTYSALGKFPRIKRTAEALQYR 717
QY 786 KETSASDVWSYGIWMMWVSYGERPYMTNDVINALTEODYRLPMDCCSALHQLMLD 845
DB 718 KETSASDVWSYGIWMMWVSYGERPYMTNDVINALTEODYRLPMDCCSALHQLMLD 777
QY 846 CMQKDRNHRKFGQIVNTLDMKIRNPNSIKAMAPLSSGILNPLDRTIPDYTSNTVDW 905
DB 778 CMQKDRNHRKFGQIVNTLDMKIRNPNSIKAMAPLSSGILNPLDRTIPDYTSNTVDW 837
QY 906 LEAIKMGQYKESFANAGTSPFVSOMMEDILRYGVTLGKOKILNSIOVMRAQNMQ 964
DB 838 LSAIKMGQYKESFANAGTSPFVSOMMEDILRYGVTLGKOKILNSIOVMRAQNMQ 896
OX
RESULT 13
EPB3_XENLA STRAND: PRT: 974 AA.
ID EPB3_XENLA
AC 091735;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
DE KINASE RECEPTOR TKC).
OS TKC.
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NC NCBL_Taxid=8355;
OX
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96068901; PubMed=7478602;
RA Scales J.B., Whinnig R.S., Renaud C.S., Shea L.J., Sargent T.D.;
RT "Novel members of the eph receptor tyrosine kinase subfamily expressed
RT during xenopus development."
RT Oncogene 11:1745-1752(1995).
CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC
CC MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
CC ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS
CC IN TESTES, KIDNEY, OVIDUCT AND PHARYNX.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
CC RECEPTOR SUBFAMILY.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; LA3620; AAA93526.1; -

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DR HSP. P29323; 1BAF.
DR InterPro: IPR000719; .
DR InterPro: IPR001090; .
DR InterPro: IPR001245; .
DR InterPro: IPR001426; .
DR InterPro: IPR001660; .
DR InterPro: IPR001777; .
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; PKinase; 1.
DR Pfam: PF00536; SAM; 1.
DR Pfam: PF01404; Eph_1bd; 1.
DR PRINTS: PR00014; ENTPEI11.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 15
FT CHAIN 1 974
FT DOMAIN 17 534
FT TRANSMEM 535 553
FT DOMAIN 556 974
FT DOMAIN 178 315
FT DOMAIN 316 423
FT DOMAIN 424 520
FT DOMAIN 609 872
FT DOMAIN 899 974
FT SITE 972 974
FT NP_BIND 615 623
FT DISULFID 60 95
FT BINDING 641 641
FT ACT_SITE 734 734
FT MOD_RES 584 584
FT MOD_RES 590 590
FT MOD_RES 768 768
FT MOD_RES 918 918
FT CARBOHYD 330 330
FT CARBOHYD 420 420
FT SEQUENCE 974 AA; 108263 MW; F881412E86628533 CRC64;

Query Match 67.7%; Score 3465.5; DB 1; Length 974;
Best Local Similarity 66.2%; Pred. No. 7.2e-207;
Matches 645; Conservative 142; Mismatches 172; Indels 15; Gaps 6;

QY 2 LAAY---EETLMDSTATAELGAMVHPSPGMEVSGYDENMNTIRTYOVGNVSESSQNMV 58
DB 11 LSAVGLLEETLMDIKWTTSLSLAWAVPDSGMEVSGYDEASNPRIPTYOVGNVRSQNMV 70
QY 59 LRTKPIRRRGAHRIHVENKFSVRDSSIPVSGCKETFNLYYEADPSATKTFPMWME 118
DB 71 LRTQPIIPQDQRYVVELKFTVRODONSPLNRGSKETEFNFYEESDSDSASDPFME 130
QY 119 NPWVYVDTIADSDSVDLGRWVKITEYRSPGSRSEYFAFDYGGCMLAVRV 178
DB 131 NPYIKVDYIADPSFSRDSG---RVNTKIRSFEPISRAFFIAPFDLGLACVSLISRV 186
QY 179 FPKRCPIRIIONAIFQETLSGAESTSLVAARGSCITANAEVDPVPIKLYCNGDGEMLVPIG 238
DB 187 FRKCRPTTAGASAPPEITITGAEPSLVIAAGTGVPMALLEVSVPLKLYCNGDGMVAVPG 246
QY 239 RCMKAGFEAVENGTVCRGCPGCTFKANOGDEACTHCGINSTRITSEGTATNCVGRNGYRA 298
DB 247 ACTCAAGFEPAKDKVQCAQCKRGTYKSGKGCSCMPCANRAISATVTCSCQNGYRA 306
QY 299 DDDPDMPTTTPSAQVAVSSVNTSLMLEWTPRODGGREDVLYNITCKSCSGGRGAC 358
DB 307 DGSATFACSTVSPASAPROVIVSNVETSVYLENAEFGHGLGSDVLYNIVICKC--LEELC 364
QY 359 TRCGDNVQYAPRQGLTEPRIVYISDLAHTQYTFEIOAVNGVDGSPSPQFASVNTITN 418

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Db	365	SRDDVNWQFPRDLGCTQRLVLSHQLQHTKTSFSLQAVNGSGSPHPIRYFTVNTITN	422
Qy	419	QAPSAVSIHQVSRFVDSITLTSMSQPODPKNCVILIDELQYER-ELSEVNAIAIKSPFN	477
Db	425	QAAPSSVPWQSHGSLANSLTSLMPPESPNCIILIDYEIKYKAGHIGAGMTVTSQRTTV	484
Qy	478	TVTGLKAGVIVFOVARFVAVAGYGRGSGKMYFQTMTEAYGTSIOEKLPIITISSAGLV	537
Db	485	RMEGMPDPIVYVQVAVARFVAVAGYASERREGQITAEIGDMSLSIQEOVPWNGSVTGLI	544
Qy	538	FLTAVVVIIVLC-NRRGFRADESEYTKLQHTSGHITPGKIXIDPFTEEDPNEAVREF	596
Db	545	FLTAVVVIIVLCSEYTSRRQRNDSSETEKLYQ---MYPGMKLYIDPFTEEDPNEAVRDF	600
Qy	597	AKEDISCKIEQVIGAGEFGEVSCGHLKLPKREIFAIKITLKSQTEKQORDPFLSEAS	656
Db	601	AKEDISCKIEEYVIGAGEFGEVSCGHLKQGRBOFAIKITLAGYTEQORDPFLGEAS	660
Qy	657	IMGQDPHNVILHEGVTKSPVWMLTEEFMENGSLDSFLRONDQGFVIOLVGLMGIAA	716
Db	661	IMGQDPHNPILIEGVVRSRPMILTEFMENGALDSPFLRNMQGFVIOLVGLMGIAS	720
Qy	717	GKKYLDADNVYVRDLAARNILVNSLVCXKVSDFLSRFLSDOTSDPYTSALCGKPIRM	776
Db	721	GKKYLSSENVYVRDLAARNILVNSLVCXKVSDFLSRFLSNSDDPYTSALCGKPIRM	780
Qy	777	TAPEAIQYRKFTSADSVSYGVIMMEVWVSGYERPYMTQDVIAMIEQYRLPPMDCP	836
Db	781	TAPEAISYRKFTSADSVSYGVIMMEVWVSGYERPYMTQDVIAMIEQYRLPPMDCP	840
Qy	837	SALHQLMDCKQKRNHRPKGQIVNTLDKIRNPNSLKMAAPLSSGINDPLDLRTIPDY	896
Db	841	SALHQLMDCKLRDNNLRPKQSQVSSLDKIRNMAASLKTSGQAGVSOQLDLRTVDPY	900
Qy	897	TSFNTVDEMLBAIKMGQYKESFANAAGTSPGVYSSQMMEDILVGVTLGHQCKILNSIQ	956
Db	901	TTFPTVSDMLEIKMGQYQENFTSAGTSHFLVAQMTAEIDLIGVTLGHQCKILNSIQ	960
Qy	957	VWRQNMQIOSEVY 970	
Db	961	DNRLOMSQTLPEVQY 974	
RESULT 14			
EPBS_CHICK			
ID	EPBS_CHICK	STANDARD;	PRT; 1002 AA.
DC	Q07497;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	EPHRIN TYPE-B RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE CEK9).		
GN	EPHRS OR CEK9.		
OS	Gallus gallus (Chicken).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OX	Gallus.		
NCBI	TaxID=9031;		
RP	[1]		
RA	SEQUENCE FROM N.A.		
RA	MEDLINE=97066069; PubMed=8909550;		
RT	Soans C., Holash J.A., Pavlova Y., Pasquale E.B.,		
RT	"Developmental expression and distinctive tyrosine phosphorylation of		
RT	the Eph-related receptor tyrosine kinase Cek9."		
RT	J. Cell Biol. 135:781-795(1996).		
RT	[2]		
RA	PARTIAL SEQUENCE FROM N.A.		
RA	MEDLINE=93288394; PubMed=8510926;		
RA	Sajjadi F.G., Pasquale E.B.,		
RT	"Five novel avian Eph-related tyrosine kinases are differentially		
RT	expressed".		
RT	Oncogene 8:1807-1813(1993).		







SEQ	SSOURCE	986 AA: 109840 MM: C3AF4078DBD3F0255-CNC64;
FT	MOD.RES	595 PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	MOD.RES	601 PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
FT	MOD.RES	778 PHOSPHORYLATION (AUTO-) (POTENTIAL)
FT	MOD.RES	928 PHOSPHORYLATION (AUTO-) (POTENTIAL)
FT	CARBOHYD	340 N-LINKED (GLCNAC...) (POTENTIAL)
FT	CARBOHYD	407 N-LINKED (GLCNAC...) (POTENTIAL)
SO	SSOURCE	986 AA: 109840 MM: C3AF4078DBD3F0255-CNC64;

[illegible]

Query Match	Score	DB 1;	Length
60.0%;	3070;	DB 1;	986;
Best Local S/m arity	60.1%;	Prod No 3 100	

best local similarity 60.1%; Pred. No. 2.1e-182;  
Matches 582; Conservative 147; Mismatches 218; Indels 22; Gaps 11.

Search completed: July 24, 2001, 16:32:38  
Job time: 204 sec

OY	4	AVEETLMOSTJATAEJGMVWHP--PSCGMEVSGYDENNMTITTYOVANVESONNNMLRTK	62
Db	28	ASEVTLLOSRSVQGEJGMIAISPLEGMEVSIIMDEKNTPIITTYOVANMESOONMLRTD	87
OY	63	FLRRGAAHRIHYEMKFSVRDCCSIPSVDSCKETFNLYYYEADPDSATKTFPMNENPV	1222
OY	123	KYDTIADESFSOVYDGLGRVWKINTEVSPBPVRSRGYLAFOYGGCMSLIAVRYFRK	1822
Db	144	KIDTIADESFQYDGLGRVWKINTEVSPBPVRSRGYLAFOYGGCMSLIAVRYFRK	2033
OY	183	CPRIIONAIFOETLSGAESTSLVAARSGCIANAEEVDPIKILCNDGDEMIYIGRCMC	2424
Db	204	CPLYRNLAOEPDITITGSDTSSILEVRSGSCVDNSEKDPV--KMYCAGDEMIYIPICGCLC	2622
OY	243	KAGFEAVENGIVCGCCPGCTRKAOGDEACHCINSRITTSSECATNCVCNRYRADLDP	3022
Db	263	NAGFEHNHG--COACKGVYKALSTAAOSCKPSPHYALREGSTCTCGRGFYADTDP	320
OY	303	LDMPCTTIPSAPOAVISSVNETSIMLEMTPEPDGSGREDLYVINICKSGSGAGCTRCG	362
Db	321	ASMPCTRPSPAPQMLISVNETSINLEMSPPONGSGRPDYSLYMLKRCGSDLTRCRPGC	380
OY	363	DNOVAPRQGLTEPRYIYISDLAHTOYTEICAOVANGVDOSPFSPQFASVNITTNQAP	4222
Db	381	SGVHSPQONLKTTKVSIYDLQAHNTYTFEEVINSINGVSKONGQOQAVSVTNNQAP	440
OY	423	SAVSIHQVSTRVOSITLSNSOPPOPPGVILDYELQYKEKELSEYNATAIKSTNT--VT	480
Db	441	STVYQIQPKDTRHSVSLIMPPEPRPGVILETEVKYKEDQONERTTYRIYKTTSRGADK	500
OY	481	GLKAGAIYFQVRRARTVAGYGRYSCKMYFQTMTEAEOXTSIDQELILIGSSAAGVFLI	540
Db	501	GLNPLTYVFEVHARRATAAGGEFSGPPEFTTNTVPSPMG--EASPTVLLVYVAGSIYV	559
OY	541	AVVVAIAYCNRR--GEPRASEYTDKLOHTTSHITTPKAKIYIDPTTYEDPNDVAREFAK	598
Db	560	VILIAAVYISRRNSKTSKAAQEADEE----KHLNQGVKTYVDPPTYEDPNOAVREFAK	613
OY	599	EIDISCVKIBOYIGAGEFGEVSGHILKPGKREIFAATILKSGYEXKOROPFLEASIM	658
Db	614	EIDASCIKIEKVIGVGEFGEVSGRLKVPKREIYVAITLKAAGYDKOROPFLEASIM	673
OY	659	GQEPHPVHILEGVYKSTPYVMTITERPMENGSIDSLTRONDOQFYIQLVGLRGIAAGM	718
Db	674	GQEPHPVHILEGVYKSTPYVMTITERPMENGSIDSLTRONDOQFYIQLVGLRGIAAGM	733
OY	719	KYLDAMNVYHRLAARILVANSMLYKVSDFGSLREFLEDOTSDPRTYSAJGKRPIMRTA	778
Db	734	KYLSDMNSYVHRLAARILVANSMLYKVSDFGSLREFLEDOTSDPRTYSAJGKRPIMRTA	791
OY	779	PELAIOYRKFTSADWVSSTGYVMEVWVSSTGERPYMDTNDVINAIEODYRLPPEMDCSA	838
Db	792	PELAIOYRKFTSADWVSSTGYVMEVWVSSTGERPYMDTNDVINAIEODYRLPPEMDCSA	851
OY	839	LHQLMLDCMQKDNHNPARGQAIYNTLDKRIIRPNLSKLAAA--PLSSGINLPLDRIPIYT	897
Db	852	LHQLMLDCMQKDNHNPARGQAIYNTLDKRIIRPNLSKLGRGLDNSSRTNTTLLDPSPPWS	911



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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:28:49 ; Search time 34.42 seconds

(without alignments)  
3728.526 Million cell updates/sec

Title: US-09-378-759-11

Sequence: 1 LLAVEETLMDSTTAETAEAG.....ILNSIQVRAQNMQIQSEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_16:\*  
2: SP\_Archaea:\*  
3: SP\_Bacteria:\*  
4: SP\_Fungi:\*  
5: SP\_Human:\*  
6: SP\_Invertebrate:\*  
7: SP\_Mammal:\*  
8: SP\_MHC:\*  
9: SP\_Organelle:\*  
10: SP\_Phage:\*  
11: SP\_Plant:\*  
12: SP\_Rodent:\*  
13: SP\_Unclassified:\*  
14: SP\_Virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5082	99.3	994	11	Q9GVY4
2	3734.5	73.0	815	13	Q57458
3	3429	67.0	938	11	O60669
4	2917.5	57.0	983	4	Q9H2V4
5	2818.5	55.1	552	4	Q9H4H4
6	2814.5	55.0	621	4	Q9H4H3
7	2723.5	53.2	987	13	Q73875
8	2691	52.6	1005	4	Q9NUA9
9	2682.5	52.4	880	13	Q73879
10	2674	52.3	976	13	Q73878
11	2332	45.6	853	4	Q9P269
12	2300.5	45.0	977	13	Q9PWR5
13	2028	39.6	1080	5	Q9Y1J0
14	2024	39.6	1047	5	Q9Y1J0
15	2017	39.4	1035	5	Q9XZL6
16	2017	39.4	1096	5	Q9Y4E5
17	1923.5	37.6	1019	5	Q9G435
18	1877.5	36.7	977	11	Q9ESJ2
19	1638	32.0	353	13	Q9PVV2

20	1623	31.7	353	13	Q9U8W2	Q9U8W2 eptatretus
21	1617.5	31.6	666	13	Q73876	Q73876 brachydantio
22	1572.5	30.7	490	13	Q73877	Q73877 brachydantio
23	1464	28.6	539	4	Q9H2V3	Q9H2V3 homo sapien
24	1422	27.8	1122	5	O61460	O61460 caenorhabd1
25	1326.5	25.9	893	5	Q9Y1Y3	Q9Y1Y3 ephydactia f
26	1311	25.6	353	13	Q9U8V9	Q9U8V9 eptatretus
27	1310.5	25.6	349	13	Q9U8W1	Q9U8W1 eptatretus
28	1299.5	25.4	348	13	Q9U8W0	Q9U8W0 eptatretus
29	1292.5	25.3	350	13	Q9PVV1	Q9PVV1 lampetra re
30	1253	24.5	323	13	Q9Y1J3	Q9Y1J3 xenopus lae
31	1252.5	24.5	919	5	Q21477	Q21477 caenorhabd1
32	1143	22.3	342	5	Q9U8V8	Q9U8V8 brachyosteo
33	1137	22.2	277	4	Q9H124	Q9H124 homo sapien
34	782.5	15.3	334	4	Q9UFC3	Q9UFC3 homo sapien
35	771.5	15.1	1362	13	Q9PDK6	Q9PDK6 xenopus lae
36	630	12.3	502	13	Q9DDK6	Q9DDK6 salmo salar
37	607	11.9	812	14	O85466	O85466 avian sarco
38	606	11.8	1504	5	Q9YV86	Q9YV86 drosophila
39	603.5	11.7	348	4	Q9UMJ5	Q9UMJ5 homo sapien
40	600.5	11.7	383	4	Q9NUA4	Q9NUA4 homo sapien
41	600.5	11.7	505	4	Q9H5Y5	Q9H5Y5 homo sapien
42	600.5	11.7	488	13	O13064	O13064 xenopus lae
43	599	11.7	1371	11	Q9QVW4	Q9QVW4 rattus sp.
44	598.5	11.6	496	4	Q9MYT8	Q9MYT8 homo sapien
45	594	11.6				

## ALIGNMENTS

RESULT 1  
ID Q9GVY4 PRELIMINARY: PRT: 994 AA.  
AC Q9GVY4:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE NEURAL KINASE, NTK-EPH/ELK/ECK FAMILY RECEPTOR-LIKE TYROSINE KINASE.  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94181250; PubMed=8134103;  
RA Henkemeyer M., Marengere L.E., McGlade J., Olivier J.P., Conlon R.A.,  
RA Holmeyer D.P., Letwin K., Pawson T.;  
RT "Immunolocalization of the Ntk receptor tyrosine kinase suggests roles  
in segmental patterning of the brain and axonogenesis.";  
RL Oncogene 9:1001-1014(1994).  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
TYROSINE PHOSPHATE (BY SIMILARITY)  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
RECEPTOR SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC HSSP: P06339; 3LCK.  
CC InterPro: IPR000561; -  
CC InterPro: IPR000719; -  
CC InterPro: IPR001090; -  
CC InterPro: IPR001245; -  
CC InterPro: IPR001426; -  
CC InterPro: IPR001660; -  
CC InterPro: IPR001777; -  
CC Pfam: PF00041; fn3; 2.  
CC Pfam: PF00069; pkinase; 1.  
CC Pfam: PF00536; SAM; 1.  
CC Pfam: PF01404; EPH\_Lbd; 1.  
CC PRINTS: PR00014; ENTYPETII.  
CC PRINTS: PR00109; TYRKINASE.  
CC PRINTS: PS01186; EGF\_2; UNKNOWN\_1.  
CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011: PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00109: PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790: RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791: RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR SMART; SM00454; SAM; 1.  
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;  
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
 SO SEQUENCE 994 AA; 110759 MW; BC6B9B12A070394C CRC64;

Query Match 99.3%; Score 5082; DB 11; Length 994;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

1 LIAAEEETLMOSTTATTAELGMMVHPSPGMEEYSGYDENMNTIRIYOVCNVESSQNMMLR 60  
 23 LIAAEEETLMOSTTATTAELGMMVHPSPGMEEYSGYDENMNTIRIYOVCNVESSQNMMLR 82  
 61 TFFIRRGARHRIHVEKESVRCSSIPSPGSKETENLYYEADFDSATITFPMMENP 120  
 83 TFFIRRGARHRIHVEKESVRCSSIPSPGSKETENLYYEADFDLATITFPMMENP 142  
 121 WKVVDITADESFQVYDGGRYMKINTFVRSRGPVSRSGFYLAFOYGGCMLIAVRYFY 180  
 143 WKVVDITADESFQVYDGGRYMKINTFVRSRGPVSRSGFYLAFOYGGCMLIAVRYFY 202  
 181 RKPRIIONGAIFQETLSGAEISTLVANGSCIANAEVDVPIKLYCNGDGEMLVPIGRC 240  
 203 RKPRIIONGAIFQETLSGAEISTLVANGSCIANAEVDVPIKLYCNGDGEMLVPIGRC 262  
 241 MCKAGEAVENGTVCGCGSGTFKANOGDEACTHCPINRSTSEGAQNVCGNGYRADL 300  
 263 MCKAGEAVENGTVCGCGSGTFKANOGDEACTHCPINRSTSEGAQNVCGNGYRADL 322  
 301 DPLDMCTTIPSPQAVISVNETSLMLEMTPPRDSGREDLVYNIICKSCSGRGACTR 360  
 323 DPLDMCTTIPSPQAVISVNETSLMLEMTPPRDSGREDLVYNIICKSCSGRGACTR 382  
 361 CGDNVOYAPRQGLTEPRRIYISDLAHQYTFEIQAVNGVTQSPSPFASVNTITNA 420  
 383 CGDNVOYAPRQGLTEPRRIYISDLAHQYTFEIQAVNGVTQSPSPFASVNTITNA 442  
 421 APASVSIIMHGVSTVDSTILMSOPPOPNVILDEYQYKEKLSYNAITAKSPNTYT 480  
 443 APASVSIIMHGVSTVDSTILMSOPPOPNVILDEYQYKEKLSYNAITAKSPNTYT 502  
 481 --GLKAGAIYVFOVRATVAGYGRYSKMYFQMTAEYQTSIOEKPLITIGSSAAGLVF 538  
 503 VQGLKAGAIYVFOVRATVAGYGRYSKMYFQMTAEYQTSIOEKPLITIGSSAAGLVF 562  
 539 LIAAVVTAICNRRGFRADSETTDKLOHTSGHITPPGMKIYIDPTEYEDPNAVEEPAK 598  
 563 LIAAVVTAICNRRGFRADSETTDKLOHTSGHITPPGMKIYIDPTEYEDPNAVEEPAK 622  
 599 EIDISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDELSEASIM 658  
 623 EIDISCVKIEOVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDELSEASIM 682  
 659 GQDFHPNVIHLEGVYTKSTPYMITTEFMENGLDSELRONDGQFTYQVGLMGLIAGM 718  
 683 GQDFHPNVIHLEGVYTKSTPYMITTEFMENGLDSELRONDGQFTYQVGLMGLIAGM 742  
 719 KYLADNMVYHDLAARNITLVNSNLCKVSPDGLSRFLEDITSDPTTYSALGKRIPIWTA 778  
 743 KYLADNMVYHDLAARNITLVNSNLCKVSPDGLSRFLEDITSDPTTYSALGKRIPIWTA 802  
 779 PEALIOYRKFTASDVWSYGIYVMEVMSYGERPYWMTNOVINAIEODYRLPPMDCPSA 838  
 803 PEALIOYRKFTASDVWSYGIYVMEVMSYGERPYWMTNOVINAIEODYRLPPMDCPSA 862  
 839 LHQMLDQWQDRNRHRRPFGQIVNTLDKMTFNPNSTKLAMAPLSSGINLPLDRIIPDYS 898  
 863 LHQMLDQWQDRNRHRRPFGQIVNTLDKMTFNPNSTKLAMAPLSSGINLPLDRIIPDYS 922

QY 899 ENTVDMELEAIKMGYKESFANAGFTSPDYVSOMMEDILRYGVTLAGHOKIILNSIQVM 958  
 DB 923 ENTVDMELEAIKMGYKESFANAGFTSPDYVSOMMEDILRYGVTLAGHOKIILNSIQVM 982  
 QY 959 RAOMNOIOSVEV 970  
 DB 983 RAOMNOIOSVEV 994

RESULT 2  
 057458 PRELIMINARY; PRT: 815 AA.  
 ID 057458;  
 AC 01-JUN-1998 (TREMELREL\_06, Created)  
 DT 01-JUN-1998 (TREMELREL\_06, Last sequence update)  
 DT 01-MAR-2001 (TREMELREL\_16, Last annotation update)  
 DE EPHB2-TYROSINE KINASE RECEPTOR (FRAGMENT).  
 GN XEPHB2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NC NCB1\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tanaka M., Wang D.Y., Kamo T., Igarashi H., Wang Y., Xiang Y.Y.,  
 RA Taniohara F., Naitoh Y., Sugimura H.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC -1- TYROSINE PHOSPHATE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 DR EMBL; AF026039; BAB94603.1; -.  
 DR HSSP; P29323; 1B4F.  
 DR InterPro; IPR000561; -.  
 DR InterPro; IPR000719; -.  
 DR InterPro; IPR001245; -.  
 DR InterPro; IPR001426; -.  
 DR InterPro; IPR001660; -.  
 DR InterPro; IPR001777; -.  
 DR Pfam; PF00041; In3; 2.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS0107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR SMART; SM00454; SAM; 1.  
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;  
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
 FT NON\_TER 1  
 FT TER 1  
 SO SEQUENCE 815 AA; 90848 MW; D36D77C498097BEE CRC64;

Query Match 73.0%; Score 3734.5; DB 13; Length 815;  
 Best Local Similarity 86.9%; Pred. No. 2,46-275;  
 Matches 708; Conservative 49; Mismatches 55; Indels 3; Gaps 2;

QY 159 GFYLAFOYGGCMLIAVRYFRKPRITIOGAIFQETLSGAEISTLVANGSCIANAE 218  
 DB 1 GFYLAFOYGGCMLIAVRYFRKPRITIOGAIFQETLSGAEISTLVANGSCIANAE 60  
 QY 219 VDVPIKLYCNGDGEMLVPIGRCMCKAGEAVENGTVCGSGTFKANOGDEACTHCPIN 278  
 DB 61 VDVPIKLYCNGDGEMLVPIGRCMCKAGEAVENGTVCGSGTFKANOGDEACTHCPIN 120

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QY 279 SRTTSGATNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPROSGG 338
DB 121 SRTTSGATNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPROSGG 180
QY 339 REDLVNIITCKSCGSGRGACTRCGDNVOYAPQGLTEPRYIYISDGLAHOTYTFEIQAVN 398
DB 181 REDLVNIITCKSCGSGRGACTRCGDNVOYAPQGLTEPRYIYISDGLAHOTYTFEIQAVN 240
QY 399 GVTDSQFSPFOPASVNIITNQAPASVIMHOVSRVDSITLSMOPPOPNVILLIDYEQ 458
DB 241 GVTDSQFSPFOPASVNIITNQAPASVIMHOVSRVDSITLSMOPPOPNVILLIDYEQ 300
QY 459 YEKELSEINATAIKSPYNT--VTGLKAGAIYVEQVARTVAGYGRYSGKMFQOTMTEAE 516
DB 301 YEKELSEINATAIKSPYNT--VTGLKAGAIYVEQVARTVAGYGRYSGKMFQOTMTEAE 360
QY 517 YOTSIQEKPLITIGSSAGLVFLIIVAVIATYCN--RGEFEADSYTYKLOHTYSGHATP 575
DB 361 YOTSIQEKPLITIGSSAGLVFLIIVAVIATYCN--RGEFEADSYTYKLOHTYSGHATP 420
QY 576 GKKTIIDPFTYEDPNEAVREFAKEIDISCYKIEQVIGAGEFGEVCSGHLKLPKREIFVA 635
DB 421 GKKTIIDPFTYEDPNEAVREFAKEIDISCYKIEQVIGAGEFGEVCSGHLKLPKREIFVA 480
QY 636 IITLKSGETEKORDELSEASIMGOFDHPNVIHLEGVYTKSTPYMITTEPMENGLSDSFL 695
DB 481 IITLKSGETEKORDELSEASIMGOFDHPNVIHLEGVYTKSTPYMITTEPMENGLSDSFL 540
QY 696 RONDQOFTVIQVGLRGLIAGMKYVLADMYVHRDLAARNTLVNSNYCVKSDGSLRFL 755
DB 541 RONDQOFTVIQVGLRGLIAGMKYVLADMYVHRDLAARNTLVNSNYCVKSDGSLRFL 600
QY 756 EDDTSDPFTYISLGGKPIRMAKAEALQYRKFTSASDVMSYGIYVMEVMSYGERPYWMT 815
DB 601 EDDTSDPFTYISLGGKPIRMAKAEALQYRKFTSASDVMSYGIYVMEVMSYGERPYWMT 660
QY 816 NQDYIMALEDDYRLPPMDCPALQMLDQWCKDRHNRKFGQIVTLDLKMIRNPSTLK 875
DB 661 NQDYIMALEDDYRLPPMDCPALQMLDQWCKDRHNRKFGQIVTLDLKMIRNPSTLK 720
QY 876 AMAFLSSGIVTLPLDRTIPDYSFNVDLWLEAIKMGQYKESFANAGFTSFVDVSGQWME 935
DB 721 AMAFLSSGIVTLPLDRTIPDYSFNVDLWLEAIKMGQYKESFANAGFTSFVDVSGQWME 780
QY 936 DILRVGYTLAGHOKKILNSIOVRAQONQIOSEYV 970
DB 781 DILRVGYTLAGHOKKILNSIOVRAQONQIOSEYV 815
```

```
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DR EMBL: U11493; AAA67925.1; -.
DR HSP: P29323; 1B4F.
DR MGI: MGI:104770; Ephb3.
DR InterPro: IPR000719; -.
DR InterPro: IPR001090; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001426; -.
DR InterPro: IPR001660; -.
DR InterPro: IPR001777; -.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00356; SAM; 1.
DR Pfam: PF01404; Eph_Lbd; 1.
DR PRINTS: PRO0014; ENTYBEL1.
DR PRINTS: PRO0109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR SMART: SM00454; SAM; 1.
DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat;
DR Transmembrane; Tyrosine-protein kinase.
DR NON_TER
FT SEQUENCE 1 938 AA; 103996 MW; 8D128CA46F19E73F CRC64;

Query Match 67.0%; Score 3429; DB 11; Length 938;
Best Local Similarity 68.9%; Pred. No. 5,4e+25;
Matches 653; Conservative 111; Mismatches 166; Indels 18; Gaps 7;

QY 31 EVSGVDEANNPTRTQYCVNFESSONMLRTKFIIRRGARIHVEKRSYVDCSSIPSYV 90
DB 1 EVSGVDEANNPTRTQYCVNFESSONMLRTKFIIRRGARIHVEKRSYVDCSSIPSYV 60
QY 91 GSKETFNLYEADFDSTKTFPNMMEPNVYKVDITIADESFSQVDGGMKINTFVR 150
DB 61 GSKETFNLYEADFDSTKTFPNMMEPNVYKVDITIADESFSQVDGGMKINTFVR 116
QY 151 SFGPYSRSGFYAFDQYGGCSLNAVRYFKRCPIIIONGAIFQETLSGASTSLVARG 210
DB 117 SFGPYSRSGFYAFDQYGGCSLNAVRYFKRCPIIIONGAIFQETLSGASTSLVARG 176
QY 211 SCIANAEYDVPILKLYCGDGEWLVPIGRCMCKAGFEAVENGTYCRGCPSTFANQDE 270
DB 177 ACIANAEYDVPILKLYCGDGEWLVPIGRCMCKAGFEAVENGTYCRGCPSTFANQDE 236
QY 271 ACTHCPINSRTTSEGATNCVCRNGYRADLDPLDMPCTTIPSAPOAVISSVNETSLMLEW 330
DB 237 PCLPCPPNSRTTSPAPASICTCHNNFYRADSDSASACTRSPRGVINSVNETSLMLEW 296
QY 331 TPBRSGGREDLVNIITCKSCGSGRGA-----CTRCGDNVOYAPQGLTEPRYISDL 385
DB 297 TPBRSGGREDLVNIITCKSCGSGRGA-----CTRCGDNVOYAPQGLTEPRYISDL 356
QY 386 AHOTYTFEIQAVNGVTDSPSPFOPASVNIITNQAPASVIMHOVSRVDSITLSMOP 445
DB 357 AHOTYTFEIQAVNGVTDSPSPFOPASVNIITNQAPASVIMHOVSRVDSITLSMOP 416
QY 446 DQPNGVILIDYEQYKELESEYNATAIKSPYNTV--TGLKAGAIYVEQVARTVAGYGR 503
DB 417 ERPNGVILIDYEQYKELESEYNATAIKSPYNTV--TGLKAGAIYVEQVARTVAGYGR 474
QY 504 SGKMYFQMTTE-AEYQSIQEKPLITIGSSAGLVFLIIVAVIATYCNRRGEFRADSETT 562
DB 475 THREFFETISBERSGAQLDQLEPLIVGSAVAVGVVVVVVATLCKRQRHGPDAEY 534
QY 563 DKLOHTYSGHATPDKTIIDPFTYEDPNEAVREFAKEIDISCYKIEQVIGAGEFGEVCSG 622
DB 535 EKLQOY----IAGMKYIDPFTYEDPNEAVREFAKEIDISCYKIEQVIGAGEFGEVCSG 590
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QY 623 HLKLPGRREIVAIKTLTKSGYTERKORDFLSEASIMGOFDHPNVIHIEGVYTKSTPYMII 682
QY 591 RLKLPGRREIVAIKTLTKSGYTERKORDFLSEASIMGOFDHPNVIHIEGVYTKSTPYMII 650
QY 683 TEFMENGSLDFLRONDQFTVIOVLGMLRGIAAGMYLADMTVYHRDLARNILVNSL 742
QY 651 TEFMENGSLDFLRONDQFTVIOVLGMLRGIAAGMYLADMTVYHRDLARNILVNSL 710
QY 743 VCKVDFGLSRLEDDTSDDPYTSLGKRPPIRMTAPAIQYRKFTSADVWSGIYVME 802
QY 711 VCKVDFGLSRLEDDTSDDPYTSLGKRPPIRMTAPAIQYRKFTSADVWSGIYVME 770
QY 803 VWSYGERPYMDTNDQVYNALIEDYRLPPMDPCPSALHQLMDQKDRNHPKFGQIVN 862
QY 771 VWSYGERPYMDTNDQVYNALIEDYRLPPMDPCPSALHQLMDQKDRNHPKFGQIVN 830
QY 863 TLDKMIRNPSLAKAMAPLSSGINPLDRTIPDTSEFTVDEMELATIMQYKSEFANA 922
QY 831 TLDKMIRNPSLAKAMAPLSSGINPLDRTIPDTSEFTVDEMELATIMQYKSEFANA 890
QY 923 FTSFVDSQMMEDILRVGVTLAGHOKILINSIQVRAQMOINOISEV 970
QY 891 FASFDLVAQMTADLRLISVTIVGHOKILINSIQVRAQMOINOISEV 938

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RESULT 4
Q9H2V4 PRELIMINARY; PRT; 983 AA.
AC 09H2V4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE EPHRIN RECEPTOR EPHA3 COMPLETE FORM.
GN EPHA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=MELANOMA;
RA Chiarl R., Hames G., Stroobant V., Maille B., Texier C., Mach B.,
RA Boon T., Coulle P.G.;
RT "Identification of a tumor specific shared antigen derived from an
RT Eph-receptor and presented to CD4 T cells on HLA class II molecules.";
RT Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF213459; AAG43576.1; -.
KW Receptor.
SQ SEQUENCE 983 AA; 110130 MW; BE04DBF958245424 CRC64;

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Query Match 57.08; Score 2917.5; DB 4; Length 983;
Best local Similarity 57.28; Pred. No. 4; 9e-213;
Matches 550; Conservative 170; Mismatches 221; Indels 21; Gaps 12;
QY 6 EETLMDSTTAAELGKMWVHPSPGWEVSGYDENMTIRTYOVNVSESSONMLRTKFI 65
QY 29 EVNLIDSKITOGELGWTISYSHGHEIISGVDEHTPIRTIYQVCVMDHSONMLRTKMW 88
QY 66 RRGARHIVHEKFSVRCSSIPSVSGCKETFNLIYEADPDSATKTFPMENPWWKVD 125
QY 89 RNSAQKIVELKFTLRDCNSIPVLGTCETFNLIYMSDDHGVK---FREHQTID 144
QY 126 TLADESSQVLDLGRYKINTEVRSFGVSRSGVYLAFOYGGCMSLIAVAVFYKRCPR 185
QY 145 TLADESSQVLDLGRYKINTEVRSFGVSRSGVYLAFOYGGCMSLIAVAVFYKRCPR 204
QY 186 IIONGAIFQETLSGAEESTLVAAAGSCIANAEVDPVPIKLYCNGDGLVPIGCKMAG 245
QY 205 TVKNLAMPDVP-MDSQSLVEVSGSVNNSKEEDPP-RMYCSTEGEMLVPIGCKSCNAG 262
QY 246 FEAVENGTVGCGCSGTFRKANOGDEACTHCPINSTRITSEGTNCVNGYRRALDLDLM 305

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DB 263 YE--ERGFMQACRPGFYKALDGNMCKACPPHSSFTQEDGSMNCCENNYFRADKDP 320
QY 306 PCTTISAPQAVISSVNETSLMEWTTPPDSCGRELVNITICKSGSRGACTRCGNV 365
DB 321 ACTRPPSPRPVINSINETSIVILDMSPDLDTGGRKDYFNITICKSGKGNITCKCEPCSPV 380
QY 366 QVAPROLGTEPRITVSDLAHQYFEEIOAVGVDSQFSPQFASVNTITNOAPSAY 425
QY 381 RELPRQGLNTVTVYDLIAHNTYFEIDAVNGVSELSPPRQFAVSTITNOAPSAY 440
QY 426 SIMQVSRVDSITLWSQDPQNGVILDELOYEKELESEFNATAIKS-PIN-TVYGLK 483
QY 441 LTIKORTSNTSLSWQEBEHNGIILDEYVYKQOQETSSTYLLRARGNVTISLK 500
QY 484 AGAIYVQVARKVYAGIGRSGCMYFQTMFAEYQNSIOEKLPLIGSSAAGLVFLAVY 543
QY 501 PDLTYVQIARAKAAG:GINSRKFEEETSPDS-FSISGESQVYMAISAVALILLTV 559
QY 544 VIAIV--CNRGRPERADSEYTDKLOHYTSGH-TFGMKIYIDPTEYEDPNEAREFAKE 599
QY 560 IYVLIGRFGCKSKHGAD---EKRLHFGHGLKPLGLRTYVDPHTYEDPTQVAHEFAKE 615
QY 600 IDISCVKIEQYIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTERKORDFLSEASIMG 659
QY 616 IDATNISIDKVGAGEFGEVCSGRLKPSKKEISVALKTLKGYTERKORDFLSEASIMG 675
QY 660 QFDHPNVIHIEGVYTKSTPYMII TEFMENGSLDFLRONDQFTVIOVLGMLRGIAAGMK 719
QY 676 QFDHPNVIHIEGVYTKSTPYMII TEFMENGSLDFLRONDQFTVIOVLGMLRGIAAGMK 735
QY 720 YLADMTVYHRDLARNILVNSNLVCKVSDFLGRLRELEDDTSDDPYTSLGKRPPIRMTAP 779
QY 736 YLSMGVYHRDLARNILVNSNLVCKVSDFLGRLRELEDDTSDDPYTSLGKRPPIRMTAP 793
QY 780 EAIQYRKFTSADVWSGIYVMEVWSYGERPYMDTNDQVYNALIEDYRLPPMDPCPSAL 839
QY 794 EAIQYRKFTSADVWSGIYVMEVWSYGERPYMDTNDQVYNALIEDYRLPPMDPCPSAL 853
QY 840 HOLMLDQKDRNHPKFGQIVNTLTKMIRNPSLAKAMAPLSSGINPLDRTIPDTSEFT 899
QY 854 YQMLDQKDRNHPKFGQIVNTLTKMIRNPSLAKAMAPLSSGINPLDRTIPDTSEFT 913
QY 900 NTVDMELEAIKMGQYKSEFANAAGTSFVDSQMMEDILRVGVTLAGHOKILINSIQVR 959
QY 914 RTTGMLNGVTAHCKELFTGVEYSSCDTIKISTIDMKKAGVYVGPQKKIISISALE 973
QY 960 AQ 961
QY 974 TQ 975

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RESULT 5
Q9H4H4 PRELIMINARY; PRT; 552 AA.
AC 09H4H4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE DJ74M1.1.1 (TYROSINE KINASE ISOFORM 1) (FRAGMENT).
GN EPHB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC Baaguley C.;
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AN035704; CAC10350.1; -.
KW kinase.
KW NON-TER
FT SEQUENCE 552 AA; 62206 MW; D643D1C857B1A3DB CRC64;

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Query Match 55.1%; Score 2818.5; DB 4; Length 552;  
 Best Local Similarity 99.1%; Pred. No. 6.3e-206;  
 Matches 547; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

422 PSANVIMHOVSRTVDSITLMSQPDOPNGVILDELOYEKEKELSEVNATAIKSPNTVT - 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 PSANVIMHOVSRTVDSITLMSQPDOPNGVILDELOYEKEKELSEVNATAIKSPNTVT 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

481 -GLKAGAIYFOVARTVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 539  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 OGLKAGAIYFOVARTVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

540 IAVVAIYCN-RRGERADSETTDKLOHTSGHTIPGKITYIDPTTYEDPNEAVEFAK 598  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 IAVVAIYCNRRRGERADSETTDKLOHTSGHTIPGKITYIDPTTYEDPNEAVEFAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

599 EIDISCVKIEOVYIGAGEFEVCSGHLKLPGRKEIFVAIKLKSQYTEKORDFLSEASIM 658  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 EIDISCVKIEOVYIGAGEFEVCSGHLKLPGRKEIFVAIKLKSQYTEKORDFLSEASIM 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

659 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRNDQGFYIQLVGMRLGIAAGM 718  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRNDQGFYIQLVGMRLGIAAGM 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

719 KYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPIRMWA 778  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 KYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPIRMWA 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

779 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNDVINAIEODYRLPPMDCPSA 838  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNDVINAIEODYRLPPMDCPSA 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

839 LHQLMDCMOKDRNHRPKFGQIVNTLTKMIRNPNSLKAAAPLSSGGINPLDRTIPDYS 898  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 LHQLMDCMOKDRNHRPKFGQIVNTLTKMIRNPNSLKAAAPLSSGGINPLDRTIPDYS 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

899 FNTVDEMLEAIKMGQYKESFANAGFTSPDYVSQMMEDILRQVTLAGHOKKILNSIOVM 958  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 FNTVDEMLEAIKMGQYKESFANAGFTSPDYVSQMMEDILRQVTLAGHOKKILNSIOVM 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

959 RAQMOIOSEV 970  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 RAQMOIOSEV 552  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6  
 O9H4H3 PRELIMINARY: PRT: 621 AA.  
 ID O9H4H3:  
 AC O9H4H3:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE DJ74M1.1.2 (TYROSINE KINASE ISOSFORM 2) (FRAGMENT).  
 GN EPHB2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Baguley C.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL035704; CAC10351.1; -  
 KW kinase.  
 FT NON\_TER  
 SQ SEQUENCE 621 AA; 69824 MW; 3DA4A10CEB04979BF CRC64;

Query Match 55.0%; Score 2814.5; DB 4; Length 621;  
 Best Local Similarity 99.1%; Pred. No. 1.6e-205;  
 Matches 546; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

422 PSANVIMHOVSRTVDSITLMSQPDOPNGVILDELOYEKEKELSEVNATAIKSPNTVT - 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 PSANVIMHOVSRTVDSITLMSQPDOPNGVILDELOYEKEKELSEVNATAIKSPNTVT 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

481 -GLKAGAIYFOVARTVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 539  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 OGLKAGAIYFOVARTVAGYGRYSGKMFQMTTEAYOTSTIOEKLPLIIGSSAGLVFL 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

540 IAVVAIYCN-RRGERADSETTDKLOHTSGHTIPGKITYIDPTTYEDPNEAVEFAK 598  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 IAVVAIYCNRRRGERADSETTDKLOHTSGHTIPGKITYIDPTTYEDPNEAVEFAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

599 EIDISCVKIEOVYIGAGEFEVCSGHLKLPGRKEIFVAIKLKSQYTEKORDFLSEASIM 658  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 EIDISCVKIEOVYIGAGEFEVCSGHLKLPGRKEIFVAIKLKSQYTEKORDFLSEASIM 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

659 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRNDQGFYIQLVGMRLGIAAGM 718  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 GQPDHPNVHLLEGVYTKSPVMIITEFMENGSLDSFLRNDQGFYIQLVGMRLGIAAGM 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

719 KYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPIRMWA 778  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 KYLADNMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYSALGKFPIRMWA 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

779 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNDVINAIEODYRLPPMDCPSA 838  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 PEAIQYRKFTSASDVWSYGIYVMEVWSYGERPYWMTNDVINAIEODYRLPPMDCPSA 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

839 LHQLMDCMOKDRNHRPKFGQIVNTLTKMIRNPNSLKAAAPLSSGGINPLDRTIPDYS 898  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 LHQLMDCMOKDRNHRPKFGQIVNTLTKMIRNPNSLKAAAPLSSGGINPLDRTIPDYS 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

899 FNTVDEMLEAIKMGQYKESFANAGFTSPDYVSQMMEDILRQVTLAGHOKKILNSIOVM 958  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 481 FNTVDEMLEAIKMGQYKESFANAGFTSPDYVSQMMEDILRQVTLAGHOKKILNSIOVM 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

959 RAQMOIOSEV 969  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 RAQMOIOSEV 551  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7  
 O73875 PRELIMINARY: PRT: 987 AA.  
 ID O73875:  
 AC O73875:  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE EPH-LIKE RECEPTOR TYROSINE KINASE RTK5.  
 OS Brachydanio rerio (zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbortinae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cooke J.E., Xu Q., Wilson S.W., Holder N.;  
 RT "Characterisation of five novel zebrafish Eph-related receptor  
 RT tyrosine kinases suggests roles in patterning the neural plate.";  
 RL Dev. Genes Evol. 206:515-531(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cooke J.E., Moens C.B., Roth L.W.A., Durbin L., Shiom K., Brennan C.,  
 RA Kimmel C.B., Wilson S.W., Holder N.;  
 RT "Eph signalling functions downstream of Val to regulate cell sorting  
 RT and boundary formation in the caudal hindbrain.";  
 RL Development 128:571-580(2001).  
 DR EMBL: AJ005026; CAA06299.2; -  
 DR InterPro: IPR000719; -  
 DR InterPro: IPR001090; -  
 DR InterPro: IPR001245; -  
 DR InterPro: IPR001660; -







QY	331	TPRRSGRREDLVNVICTKSCGSGRAGCTRCGDMVQAPRQGLGTEPRITISDLAHAY	390
Db	294	SPPLSSGGRRDITITNVCKQCVDRPTQRCSRGCDVRYSPRLSTRSTRVAVHQLAHNTN	353
QY	391	TFEIOAVNGVTDSPFPSPFQFASVNTITNOAPASAVSITMHOVSRTVDSITLSMSQDPQNG	450
Db	354	TFQIWAIVNGVSKHNPSPQAVSVTLITNOAAPSVMSVQSKDITRHITLAFMQPKFPNG	413
QY	451	VILDYELQYERKEELSEYNATIKSPPTN--VTGLKAGAIYFQVRRATVAGTRYSGKAT	508
Db	414	VILEYEVYVYERKDDNERKYRIVKTKTSRNADIKDITPLTSTVFVFNHARTAGYDFFSAPPE	473
QY	509	FQMTT-EAEYQTSIOEKLPLITIGSSAGLVEFLIIVVYIAIVCNRRGPERADSEYTDKLOH	567
Db	474	FSTNTVAPRVVGVMSAVLLILVAGCVVLLILITLITITRR-----SKYS-KTQO	526
QY	568	YTSGHITPGMKIYIDPTEYEDPNEAVREPAKEIDISCVKIEQVIAGAGEGVCSGHILP	627
Db	527	GEDKNVQGVGVYIDVPFTEYEDPNOAIEEPFAKEINTSCIKTEKYIGICEFEGVCSGRILP	586
QY	628	GKRLEFVIAIKTLKSGYGEKORBDLSASIMGODPHNVIHLGGVYTKSPVMTITPEME	687
Db	587	GKRLEICVAIKTLKAGFTBQQRDLPLDSASVYIGQDHPNIIHLGGVYTKCPVMTITPEME	646
QY	688	NGSLDSELRQNDGQFTYIQLVGMRLGIIAGMKYLAIDNNVYHRDLAARILVNSNLCKYS	747
Db	647	NGSLDMELRKNDCKFFTYIQLVGLIRGIASGKKYISDMSVYHRDLAARILVNSNLCKYS	706
QY	748	DGFSRLFEDTSPDPTYSALGSKFPIRMTRAPALQYRKTTSADVMSVGIYVMEVMSYG	807
Db	707	DGFSKRVLEDE-PEGAYITTR-GGKIPILRMTRAPELITRYKFTTSASDVMSVGIYVMEVMSYG	764
QY	808	ERPYPWDTNDQVINALIBODYRLPRPMDCCPALHQLMDCKQKORNNRPKFGQIVNTLDM	867
Db	765	ERPYPWMSNDQVINKAIEEGRYLRPRPMECPPLAHQLMECMRRADRPKRKSQIVNNLDM	824
QY	868	IRNNSLKLAAAPLSSGINTPLDRTIPDY--SPNTYDEMLEIKKGQYKESRANA	921
Db	825	IRNPATLTKRAGASRSHSPSTINHAPSECSAPSISAYDMLKLILGEQYREMENTA	880
RESULT	10		
ID	073878	PRELIMINARY;	PRT; 976 AA.
AC	073878;		
DT	01-AUG-1998 (TREMBLrel, 07, Created)		
DT	01-AUG-1998 (TREMBLrel, 07, last sequence update)		
DT	01-MAR-2001 (TREMBLrel, 16, last annotation update)		
DE	EPH-LIKE RECEPTOR TYROSINE KINASE RTK8.		
GN	RTK8.		
OS	Brachydanio rerio (Zebrafish) (Zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
OC	Cypriniformes; Cyprinidae; Rasbora; Danio.		
OX	NCBI_Taxid=7955;		
RN	11]		
RP	SEQUENCE FROM N.A.		
RA	Cooke J.E., Xu Q., Wilson S.W., Holder N.;		
RL	Dev. Genes Evol. 206:515-531(1997).		
RN	12]		
RP	SEQUENCE FROM N.A.		
RA	Darbin L., Brennan C., Shioml K., Cooke J., Barrios A.,		
RA	Shanmugalingam S., Guthrie B., Wilson S., Lindberg R., Holder N.;		
RL	Submitted (MAY-1998) to the EMBL/Genbank/DBD databases.		
DR	EMBL; AJ005029; CAA06302.1; -		
DR	HSSP; P00523; 2PTR.		
DR	ZFIN; ZDB-GENE-990415-65; rtk8.		
DR	InterPro; IPR000561; -		
DR	InterPro; IPR000719; -		
DR	InterPro; IPR001090; -		
DR	InterPro; IPR001245; -		
DR	InterPro; IPR001660; -		
DR	InterPro; IPR001777; -		

DR Pfam; PF00041; fn3\_2.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00536; SAM; 1.  
DR Pfam; PF01404; EPH\_1cd; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD001495; -; 1.  
DR PROSITE; PS01186; EG2\_2; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR SMART; SM00454; SAM; 1.  
KW ATP-binding; EGF-like domain; Glycoprotein; Transferase.  
KW Tyrosine-protein kinase.  
SQ SEQUENCE 576 AA; 108180 MW; 46197554A38B0B1E CRC64;

Query Match	52.3%;	Score 2674;	DB 13;	Length 976;
Best Local Similarity	54.5%;	Pred. No. 1.6e-194;		
Matches 529;	Conservative 164;	Mismatches 245;	Indels 32;	Gaps 16

QY	58	MLRTEFIRRGHNRHRYHMKCSVNRCCSIPBVPSCKEFUYLYVEDFDSATTEPMM	11
Dd	78	MLRTEFIRRGHNSOYVYIRTEHMECSAMPSEFTCKTEFMYLYIQSDDEIATSTHPMM	13
QY	118	ENPMVKVDTLADESFESOVDLGGRVAKINTEVRSFPGVSRSGFYLAQDYGCCSLIAVR	177
Dd	138	ENPMYSKVDVTVADEFLLR---GGERKSNVTKVRGPISTLGEFLAETOAGCMAALLSVR	193
QY	178	VEYRCPTIONGAIPORTLGSASTSLY-AARSCJANAE---EVDVPIKYONGGEM	233
Dd	194	VFEKKCPAVNSAFSEFPETL----PHSLVQOABEVCYDNSAPTOQCTAPPMFEGEDGOM	249
QY	234	L-VPIGRMCKAGEIVENGTVCRQCPSETPKANQOGDEACTHCEINRSTTSSEGATNCVCR	292
Dd	250	VGPPESTCACRGEYEPVDSR-CRACGLGQYKASVGSGLCVCPCDNSHTHAGSLCYCR	300
QY	293	NGXYRADLDIPDMCCTTIPSAPOAVISSVNTSISMLETPPRDSGGREDLYNITCKSCG	353
Dd	309	PGRHAIASDLPDSACTPPSPAKRSITITQINDTVTLTESEPLDGGSDSLSYVECHNC-	367
QY	353	SGRGA-CTRCGDANOYAPROJGLEPRTIYSDLLAHTQYFEIOAVNGVTDQSPFSQFA	411
Dd	368	--RSLCVOQCADSITYRRGQGVSGRVIITGLLPHITTYFTVLAQNGVSAVSHTPASS	422
QY	412	SVNITTNQAPSAVSIJHQSRYVDSITLSMSQDPQPNGLVLDIETOYKEELSE-YNAT	470
Dd	426	SVNITTSRDVAVPASGIRRIKASSSVSIISMTVPQOHSJODVOLTYSLSKGODGDMQYV	485
QY	471	AIKSPVTMTLKGALYVFOVARFATYAGRYSGKNYFOHTEAEYOTSIOEKLPLIG	530
Dd	486	SSRSSVYVNDLSAKSOYQOYVRRKRTAAGICHSESAVSIISLPDEDSPP--RLMLTV	542
QY	531	SSAAGVELLAIVAVIATVCRNGFERADSEYTDKLOHTYSGHITTPGKKIYIDPTYEDPN	590
Dd	543	LVAIGLLILIAIVIAVAFCEFRSTRRRDDP--PDKSCQFIMQO--GIKYVIDPTYEDPN	598
QY	591	EAVREPKIEDISQVITEOYVIGAGEEPEVCSGHKJLPGKREIPAIKTLKSGTEKORD	650
Dd	599	EAVREPKIEDIVSFVKTIEVYIGAGEEPEVCGRLKYGKKEENVAIKTLKGTTDKORD	658
QY	651	FLSEASIMGQFDHBNVTHEGVTYKTPVNIIEFPMNGSISDLSFLRONDQOFVIOJVM	710
Dd	659	FLSPASIMGQOHNPIHLEBGVITASCQVMIITFEYMEGALDPSRLRNDQOFPIPIJVM	718
QY	711	LRGIAAGKVIADMNVYHRDLAARNILVNSNLCKYKSDFGLSRPLEDTSIDPTYSAJG	770
Dd	719	LRGIAASCKKYLSEMSVHRDLAARNILVNSNLCKYKSDFGLSRPLETENSIDPTYSTSLG	778
QY	771	KFPIRMVAPPAEAIQYRKTSAADSWYSYGIWMEVMSYSGERYPMNTODVYNALTEOYRLP	830

Db	779	KIP1MTWPEELIAERKFTTSADVNSIGIVMEVNSFGERRPMDSNODYNALTEODTRLR
Oy	831	PMDQPSALHOLMLDMCQKDNRNHPKFQGYINTLDDKMIIRNPNSLKAAAPLSSGINPLLD
Dd	839	PPPECPASLHQLMDCMQCKEKSSRPICALYSAIDRLIRNPASIKITGRIPDGGSHPLD
Oy	891	-RTIPDYTSFNTVDLEWLAIKMGQIKESFANAGTSEFDVVSOMMEDILRGVTTLACHOK
Dd	899	ORAPPPLSLCHSCSVADMRLRAIKMERVEDAFMQAGFTTAIOHTIHISTEDLLRIGVTLACHOK
Oy	950	KILNSIQVMR 959
Dd	959	KILLSVOFLR 968
 RESULT 11 O9P269 PRELIMINARY; PRT; 853 AA.		
Id	O9P269	
Dt	01-OCT-2000 (TREMBLrel. 15, Created)	
Dt	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
Dt	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
De	KIAlA1459 PROTEIN (FRAGMENT).	
Gn	KIAlA1459.	
Os	Homo sapiens (Human).	
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Oc	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
Ox	NCBI_TaxID=9606;	
Rn	[1]	
Rx	SEQUENCE FROM N.A.	
Rf	MEDLINE=20277482; PubMed=10819331;	
Ra	Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;	
Rt	"Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";	
Rl	DNA Res. 7:143-150(2000).	
Cc	-1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN TYROSINE PHOSPHATE (BY SIMILARITY).	
Cc	-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).	
Cc	-1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.	
Cc	-1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.	
Cc	EMBL; AB040892; BAA95983.1; -	
Dd	InterPro: IPRO00561; -	
Dd	InterPro: IPRO00719; -	
Dd	InterPro: IPRO01245; -	
Dd	InterPro: IPRO01426; -	
Dd	InterPro: IPRO01660; -	
Dd	InterPro: IPRO01777; -	
Dd	Pfam: PF00004; fn3_2.	
Dd	Pfam: PF00069; pkinase; 1.	
Dd	Pfam: PF00536; SAM; 1.	
Dd	PRINTS: PR00014; ENTPEITI.	
Dd	PRINTS: PR00109; TYRKINASE.	
Dd	PROSITE: PS01186; EGF_2; UNKNOWN_1.	
Dd	PROSITE: PS00107; PROTEIN KINASE_ABP; 1.	
Dd	PROSITE: PS00011; PROTEIN KINASE_DOM; 1.	
Dd	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.	
Dd	PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.	
Dd	PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.	
Dd	SMART: SMO0060; FN3; 1.	
Kw	AAT-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Transferrase; Transmembrane; Tyrosine-protein kinase.	
Kw	NON_TER 1	
So	SEQUENCE 853 AA: 94149 MW: 7248501BFB855002 CRC64;	
 Query Match 45.6% Score 2332; DB 4; Length 853; Best Local Similarity 51.7%; Pred. No. 1.4e-168; Matches 446; Conservative 153; Mismatches 221; Indels 42; Gaps		
Oy	132	SFSQVLDGGRVAKINTEVERSGPVSRSGFYLAPODYGGCSNLAVRYFKRCPIIONGA 19UD

Db	1	SETGADLVVRRLKLTETVRSVGPLSKREFYAFODIGACIALILSLRIYKPCPMAYNLA	60
Qy	192	IFOEFLSAESTSTLVAAGSGESTIAAAEEDVAYIKLYCNGDEGMLPIORCKAKAEAVEN	251
Db	61	AFSEAVATGADSSSLVEVAGQCVRHLEEDTP-KMYCSAEGEMLVPICKYCSAGYE--ER	117
Qy	252	GTVCRCGCSPTGFKANQGDGEACTHCPINSRTTSEGATNCVCNRYGRADLDPLDPCCTIP	311
Db	118	RDACVACELGFKASQAPDQLCARCPRHSHSAAPAQAQCHDLSYRAALDPPSSACTRP	177
Qy	312	SAPQAVISSVNETS.LMLEWTPRRPSGCHREDLVYIICKSCSGGACTRCGDNVQYAPRO	371
Db	178	SAPVNL.ISSVNGTSTVLEMAPRLDPGGKSDITYNAVRCRPMALSRCAAGSGTRFVPOQ	237
Qy	372	LGTPEPRYISDLAHQYTFEIDAVNCTPQSPFSPOPASVNTTQOAPSAVSIHNOY	431
Db	238	TSLVASLIVALLAHMNYSEWIEVNVGSDLSSEPPRAAVYNTTQOAPSOVVYROE	297
Qy	432	SRTVDSTLSMOPDQPNGVILDELOYEKEKLESEYNATAIKSPFN--TYTGKAGAIYV	489
Db	298	RAGQSVSLTLMQEPQPGRIILLEYEIKYKEDKMOSYSLTKATTPATVAYSGLKGRIYV	357
Qy	490	FOVRRATVYAGTGRISGKKYFOT---MTEAEQYSIOEKLPLITGSSAAGLVFLIAYVYA	546
Db	358	FOVRRATVYAGTGRISGKKYFOT---MTEAEQYSIOEKLPLITGSSAAGLVFLIAYVYA	546
Qy	547	IYCNRR--GFERADSEYTDKLOHTSG-----HTRPGM----KIYIDPTYEDPN	590
Db	409	LICKRHGQSKAFQDSDSEKMHITONGAPRPVFLPLHHPGKLPEFOFYAOPHTTEEPG	468
Qy	591	EAVRFEAKEIDISCVKLEDOVYAGAEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORD	650
Db	469	RAGRSFTREIEMASRIHIEKIIIGSDSGEVCGR.LRVPGQGRVPAIKALAKAGTYERORD	528
Qy	651	FLSEASINGQDPHNV.IHLEBVTKSTPVM.IITEFMENGSLDSTLRONDQFTVYIOLVGM	710
Db	529	FLSEASINGQDPHNV.IHLEBVTKSTPVM.IITEFMENGSLDSTLRONDQFTVYIOLVGM	710
Qy	711	LRGIAAGKTYLADNMVYVRODLAANIILVNSLVCVKVDFGLSRLEEDTDPPYTSALG	770
Db	589	LRGVAGKRYTSLDGLYVRDLAARVVLDSNLVCVKVDFGLSRLEEDD-PPAAVTTT-GG	646
Qy	771	KPFIWMTAPEALIQYKFFPSASDVNSYGIYVMENWASYCERPMQDNTODVYINALEODYRLP	830
Db	647	KPFIWMTAPEALAPFTESASDADWSFGYVMMEVLAIGERPYKMNNTNDVYISSVEGRRLP	706
Qy	831	PRMDCPSALHQLMLDWCOKDRNHRPKFEGQIVNTLDKMI.RNPNSLKAAAPLSSGGINPLLD	890
Db	707	APMGCPALHQLMLDWCOKDRNHRPKFEGQIVNTLDKMI.RNPNSLKAAAPLSSGGINPLLD	890
Qy	891	RTIPRTYSFN-----TYDLEMLEIAIKMQYKESAPNAGFTSFEDVSOHMMEDILRVGTL	944
Db	766	RSCFPLRGSGGGGGLVGDWLDLSIRMGRYDRHFAAGYSGLGVLRMNAQDVRAALGITL	825
Qy	945	AGHOKKILNSIQVMAPOANOJO 966	
Db	826	MCHOKKILIGSTOTRAOULTSQ 847	
RESULT 12			
Q9PMRS			
ID	Q9PMRS	PRELIMINARY:	PRT: 977 AA.
AC	Q9PMRS		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	EPH RECEPTOR TYROSINE KINASE PRECURSOR.		
GN	EPHA2.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;		
OC	Xenopodinae; Xenopus.		

OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99077686; PubMed=9858686;  
 RA Hebling P.M., Tran C.T., Brandt A.W.;  
 RT "Requirement for EphA receptor signaling in the segregation of Xenopus  
 third and fourth arch neural crest cells.";  
 RL Mech. Dev. 78:63-79(1998).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 TYROSINE PHOSPHATE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 RECEPTOR SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 FIBROBLASTIN TYPE III-LIKE DOMAINS.  
 DR EMBL: AJ002493; CA05500.1; -  
 DR HSSP; P08631; 1AD5.  
 DR InterPro; IPR000561; -  
 DR InterPro; IPR000719; -  
 DR InterPro; IPR001090; -  
 DR InterPro; IPR001245; -  
 DR InterPro; IPR001426; -  
 DR InterPro; IPR001660; -  
 DR InterPro; IPR001777; -  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR Pfam; PF01404; EPH\_1bd; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD001495; -; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V; 2; 1.  
 DR SMART; SM00454; SAM; 1.  
 DR AT-Blinding; Glycoprotein; Kinase; Phosphorylation; Receptor; Signal;  
 KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 977 EPH RECEPTOR TYROSINE KINASE.  
 FT SEQUENCE 977 AA; 109593 MW; 9931C19031A55F1D CRC64;

Query Match 45.0%; Score 2300.5; DB 13; Length 977;  
 Best Local Similarity 48.2%; Pred. No. 4.4e-166;  
 Matches 463; Conservative 161; Mismatches 313; Indels 23; Gaps 14;

QY 1 LLAAYETLMDSTVATYAEIGMNVHP-PSGWEEVSGYDENMNTIRTYOYCNVESSQNNML 59  
 DB 22 VLOREVVLLDEKTOGELGMLTHPYGKMDLQNV-MNGSLITYVCSVQEGQDNL 80  
 QY 60 RTKFRRGARHINHEMFVSVDSSISVPSCKETNLYYEEDPSATTFENMKN 119  
 DB 81 RTNMLYRSEAHGIFELKFTYVDCNSFPGSGCTKETNLYMESDIDYGT---NFQKR 136  
 QY 120 PAVKVDITAADESFQVLDGRVAKINTEVRSFGVSRSGFLAODYGGCMLAVRYE 179  
 DB 137 QPKRIDTIAPDITYPAPFASRNKVNVEKRSYGALSKRGFLADIDGACVALLSVRIY 196  
 QY 180 YRKCPRIITNGAIFQETLSGAESTSLVARSGCIANAEEV--DVDIKLYCNGDEMLVPI 237  
 DB 197 YKCPVYVQAGMAQPEETVAGADSGIARVSGCANNNAVSVNDDP-TJHNCNDGEMLVPI 255  
 QY 238 GRCKKAEFEAVENCTVGRGCPSTGFKANOGDEACTHCPINRTSSEKATNCVANGIYR 297  
 DB 256 GHCLQPGYEV--GDTQACQPGFYSKTSNGPCQLPDHTEPSSQATPCPCMDGFER 313  
 QY 298 ADIDPDMPTTIPAPQAVISVNETSLMEWTPPRDSGGREDLVYNIICKSCSGSGGA 357  
 DB 314 STDPSSDPCTSPFASRDITAVLDGSKVLMRLPSPNSGGRSDITTYVTECKKCPASE 373  
 QY 358 CTCRCGN-VQYAPROLGLTEPRIYISDLAHTQYTFEIQAVNGVTDGSPSPQFASVIT 416

DB 374 CTPODHSNIRESENDLEKGTITIMDLEPHLNTSFTEARNGVSG-SGSSRSYATLRIS 432  
 QY 417 TNOAPPSAVSITHOVSKRVVDSTLTLSMQDPQNGYIIDYEIQYER-ELSEYNTAIRSP 475  
 DB 433 INQTEPPVYVTEFTLDNGSTLSMSVPPROQIRKVMYETEYTSKHPDANSISVORCGN 492  
 QY 476 TWTYGLKAGAIQVQVAVRQVAGRGSRGKMYEQTWTEAEYOTSIOEKLPLIGSSAAG 535  
 DB 493 SVTLKLKPLGTYTVVAVQALQDEGVGYSRDEFEFTLVEE-----SSNKAAVIGGALAG 547  
 QY 536 LVELLAVVVAIVACNRKQPERADSEYTKLOHYTSGHITTPGKAIYIDPFTTEDEAVRE 595  
 DB 548 SI-IIAIFGVGVIIEHRRRRRNPNINISESDIYFSKPDOLKPLKTYVDPTHYEDPKKAVLK 606  
 QY 596 FAKEDISCVKEQYVIGAGEGVCSSHLKLPGRKEITVAIKTKSGYTEKORRDLSEA 655  
 DB 607 FTMRPRTPSRKKNVIGAGEGVEVFKGLKLPKKESTVAIKTKLAGTEKORRDLSEA 666  
 QY 656 SIMGQDPHPNVTHLEGVYTKTPVMIITEFMENGSLDSFLQNDGQFTVIOLVGLRGIA 715  
 DB 667 SIMGQFCHNIIRLES-WSKYPKMIIVTEHMEGALDKFLKNDGSEFPIQVGLRGIA 725  
 QY 716 AGKYLADMTYVRDLAARNILVNSLVCKVSDGSLRFLDDTSDPYTSALGKFP 775  
 DB 726 AGKYLSEMYVHRDLAARNILVNSLVCKVSDGSLRFLDDTSDPYTSALGKFP 783  
 QY 776 WTAPPAIYRKFTSADVWSYGIWMEVMSYGERPYMTNDQVYNALTEQDYLPRPMD 835  
 DB 784 WTAPPAIYRKFTSADVWSYGIWMEVMSYGERPYMTNDQVYNALTEQDYLPRPMD 843  
 QY 836 PSALQLMLDCQKDRNRPFGQIVNTFLDKMIRNPNSLKKMAPLSSGINPLDRTIPD 895  
 DB 844 PSAILQLMLDCQKDRNRPFGQIVNTFLDKMIRNPNSLKKMAPLSSGINPLDRTIPD 903  
 QY 896 YTSNTVDEWTEAIKAGYKESFANAGFTSPDVVSQMMEDILRYGVTLAGHOKILNSI 955  
 DB 904 GMPEFTIEMWDSIMQGYTFEFMASPYNSMDKIILMQEDIKHIGIRQTHOKRIAPSI 963

RESULT 13  
 ID 09Y1J0 PRELIMINARY; PRT; 1080 AA.  
 AC 09Y1J0;  
 DT 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)  
 DE EPH RECEPTOR TYROSINE KINASE.  
 GN EPH OR DEK OR CG1511.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99286310; PubMed=10356296;  
 RA Scully A.L., McKeown M., Thomas J.B.;  
 RT "Isolation and characterization of Dek, a Drosophila eph receptor  
 protein tyrosine kinase.";  
 RL Mol. Cell. Neurosci. 13:337-347(1999).  
 DR EMBL; AF132028; AAD38508.1; -  
 DR HSSP; P00523; 2PTK.  
 DR FLYBase; FBgn0025936; Eph.  
 DR InterPro; IPR000561; -  
 DR InterPro; IPR000719; -  
 DR InterPro; IPR001090; -  
 DR InterPro; IPR001245; -  
 DR InterPro; IPR001660; -  
 DR InterPro; IPR001777; -  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR Pfam; PF01404; EPH\_1bd; 1.

DR PRINTS: PR00109; TYRKINASE.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE: PS0107; PROTEIN\_KINASE\_ATP\_1.  
 DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM\_1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR\_1.  
 DR SMART: SM00454; SAM; 1.  
 DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.  
 DR SEQUENCE 1080 AA; 121505 MW; 314DC3322DC89 CRC64;

Query Match 39.68; Score 2028; DB 5; Length 1080;  
 Best Local Similarity 42.18; Pred. No. 2.8e-145;  
 Matches 440; Conservative 162; Mismatches 322; Indels 120; Gaps 26;

QY 2 LAAEETLMDSTTATAEGLMNVHP-----PSGWEVSGYD-ENMNTIRTYQVCNFEES 53  
 DB LAHQDOVLLDTREATLEMTREYFGPOAQTSGWVESEFTDFVGIMN-RSYVVCDAVYH 137  
 QY 54 SONMMLRTKFRRGANHHHEMKFSVRDCSSIPSQSCETENLYYEADPFSAIKTF 113  
 DB NVNMWMSPFIDRGSANMLYIEIOTINDCSLFPGNMLSCETESLTFYE--FDAATREP 195  
 QY 114 PMNENPMVKYDTIAADES-FSQ--VDLGGFVAKINTEVSRFGPSRSGFYLAFOGYG 169  
 DB PPMQTDYSRLIARLAAGGRNOSVDV-----INTEVSLA-VNKKGYFFRDOGA 247  
 QY 170 CMSLIARVRYRCKPRITQNGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNG 229  
 DB CISVLAAYVYITCPTAVTEFAHNETPTGRIETIIEKONGCTVDNAEPYETPYL-CKG 306  
 QY 230 DGEMLVPIGRMCKAGFEAVENGTVCGSGCTFRKANOGDACHHCINSTTSEGATNC 289  
 DB DGMKTILTGCRCKAGTEPNTNKTCECPGTGKSEPVTK-CPPCPNNSAKXTGSPFC 365  
 QY 290 VCRNGYRADLPDLMCTTIPSAF-QAVISSVNETSLMLEWTPRRDSG----- 338  
 DB KCAGGYRHPMDGHRMPCYSPAPATNLTLFVDTGSAIISMSPANKNESSTENKITY 425  
 QY 339 REDLVYNIKSCSGSGACRCGDNDQYAPRQLGTEPRIYISDGLAHQYTFEIOAVN 398  
 DB HSDIVYKI-----KCNICSPNVVYNPSTDTFNETKITLNLPEPVYTYVQIHAIN 475  
 QY 399 GVTQSPFSPOF-----ASVNTITNOAPSAVS 426  
 DB SVSHINEFKRNSNSSLVANSVDIYFSNTSLNPLDLNEVKYTGAEIVFTTESVLLSTVP 535  
 QY 427 IMHOVSFTVDSITLMSOPDPNGVILDELYYER-ELSEYNATAI-KSPNTVTYGLK 483  
 DB NLRIATITNDADLEMDKPVQSDPDLFEYERMPKVELDAINKSALNTRKETAHIYGL 595  
 QY 484 AGATVFOVARATVAGYGRYSGKMYFOTME--AEQTSIQEKLPLITGSSAGLVPLIA 541  
 DB ENTGEGVQVCKTNNGFSSNMUYAQTLOVSGVYDDSVQ--IRTAGAIVTGVLVLI 653  
 QY 542 VVYIAVCNRRGERADSEYTDKLOHTSGH-----TP--CMKIYIDPFY 586  
 DB FIATVYEMR-----SKHODDLKSKTNHPLPLDYASNEVTTPLFGNSRSRVDPHTY 706  
 QY 587 EDPREAVREPAKEDISCVAIEOYIGAGEGECVSGHLKIPGK-REIYVAITLNGSYT 644  
 DB EDPQAIREFAREIDAVYITIEAIIIGGEGEDVCGRRLKIPPFVODIDVAITKLKPGSS 766  
 QY 645 EKORADFLSASIMGOFDHNVTHLEGVYTKSPVMTITFEMNGSIDSLRONDQFTV 704  
 DB EKARCDLTASTIMGOFDHNVYILOGCVTRSPVMTITFEMNGSIDSLRONDQFTV 826  
 QY 705 IQLVGLRGIAAGMKYLDAMNVYHRLAARNILVNSNLVCVSDFGISRLLEDSTDPY 764  
 DB IQLITMLRGIASGYSYLSDMNVYHRLAARNVLYNQLICKIADFGISRIEN--ASDAY 884  
 QY 765 TSLAGGFFIRMTAPALIOYRKETSADVWSYCTVMMEVWSYGERPYWMDTNDVNAIE 824  
 DB TTR-GGKIPIRMTAPALIAIRKETSADVWSYGVVIMVWSYGERPYWMSNODVIAKISIE 943

QY 825 QDVRPPMPCPSALHOLMLDMCKDRNHRPKFCQIYVNTLDMKIRNPNSLKAMAPLSSGI 884  
 DB KGYLPPMPCPSALHOLMLDMCKDRNHRPKFCQIYVNTLDMKIRNPNSLKAMAPLSSGI 1003  
 QY 885 NLPLDRTIDYTSFNTVDLEAIKMGQYKESFANAGTSPFVDSQMMEDILRVGVTL 944  
 DB GNHILDCQ-RGQNFIFSTDLMEHIKMSRCHHEKANLINAOISLRTMOOLSDMKITL 1062  
 QY 945 AGHOKITLNSIQVRAQMOINOISY 968  
 DB VGHOKITLH-----QAROLDIT 1079

RESULT 14  
 ID 0917D4 PRELIMINARY; PRT: 1047 AA.  
 AC 0917D4;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE BPH PROTEIN.  
 GN BPH OR CG1511.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,  
 RA Branton R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkeva D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahle C., Davernport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Krevitz S., Kulp D., Lai Z.,  
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Modarity C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K.C., Remington K., Saunders R.D.C., Scheller F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitzkas R., Tector C., Turner C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weisslock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003843; AAC21122.1;  
 DR InterPro: IPR000561;  
 DR InterPro: IPR000719; -

DR InterPro; IPR001090; -  
 DR InterPro; IPR001245; -  
 DR InterPro; IPR001660; -  
 DR InterPro; IPR001777; -  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00336; SAM; 1.  
 DR Pfam; PF01404; EPH\_1bd; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50013; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR ATP-binding; Transferase; Tyrosine-protein kinase.  
 KW SEQUENCE 1047 AA; 117945 MW; 44DF628CF90C4571 CRC64;

Query Match 39.6%; Score 2024; DB 5; Length 1047;  
 Best Local Similarity 42.0%; Pred. No. 5.4e-145;  
 Matches 439; Conservative 163; Mismatches 322; Indels 120; Gaps 26;

QY 2 LAAVEETLMDSTTATAEELGMVHP-----PSGMEVSGYD--ENMNTIRTYQVCNVFES 53  
 DB 46 LAHADVVLDTTREATLEMTTRPYGQAOTPGWVEESTFDEYKGINW-RSYVCDVAH 104  
 QY 54 SONNMLRTKFIIRRGARHRIHVEKESVROCCSIPVSGCKETFNLYYEADPDSATKTF 113  
 DB 105 NVNNMLMSFIRGSGANRRIYIEIOTIRDCSLFPGNALCKETFFSLFYE--FDAATREP 162  
 QY 114 PNMENPMKVKDTIADES-FSQ--VDIGRYMKINTFVRSRGPYSRSGFYLAPODYG 169  
 DB 163 PPMQTSYRIAIAGEGRFNONSVD-----INTFVKSLA-VNKGYVFAFQDGA 214  
 QY 170 CMLIAVRYEYRKCPIIIONGALFOETLSGAESTSLVAARSGCIANAEEVDVPIKLYCNG 229  
 DB 215 CISVLAVKYYITCPAVTENFAHNETPGREITITIEKONGTCVDNAEYETPTVY-CKG 273  
 QY 230 DGMVLPIGRCKAGFAEVENCTVGRGCSGCFKANODGACTHCPINSRTSECATNC 289  
 DB 274 DGMVTLTGCCRKAGYEPNVTNKTCTECLGFFKSEVTK-CTPCPPNSMNAKSTGSPFC 332  
 QY 290 VCRNGYRADLDLPDMPCTTIPSAQ-AVATSSVNETSLMELWTPPRDSG----- 338  
 DB 333 KCASGFYRHNDGRHMPCKSPAPATNLTLFVDTSATISMAKPAKNESEFSETSKIT 392  
 QY 339 REDLVYNIICKSCSGRGACTRCGDVQVAPRQLGITERPIYISDLAHQYFELQAVN 398  
 DB 393 HSDIYVKI-----KCNICSPNVVNPSTDTFNETKITLTLEPVTYTVQIHA 442  
 QY 399 GVDPSFSPQF-----ASVNTTNOAASAVS 426  
 DB 443 SVSHINEFKHSHNESSIVAVSDIVFSNTSLINPLDNEKTAQOAEIVFTTESVLSTYF 502  
 QY 427 IMHOVSRTVDSITLWSQDPQNGVILDELOYER-ELSEYNATAI--KSPNTVTGLK 483  
 DB 503 NLRIATITNKDADLEMDKPYQSDPLEFYEVRWPKELDAINKSLMNETKAHIVGLL 562  
 QY 484 AGAIYFOVARIVAGYGRSGMYQOTME--AEYQTSIQEKLPIILIGSSAGIVFLA 541  
 DB 563 ENTREYGVCKTNGGSGYSNMIVATQLOSAGSVYDSDVO--IRFAGIYIVGVLEVI 620  
 QY 542 VVYIAVCNRRGEFADSEYTDKLOHTSGH-----TP---GMKTYIDPTV 586  
 DB 621 FIATAYEYEM-----SKHODDLKSKTNHLPPLDYASNEVTTPLFGSRSYVDPTV 673  
 QY 587 EDPNEAVREPAKIDISCVKIEOVIGAGEGEVCSGHLKIPGK--REIFAITTLKSGYT 644  
 DB 674 EDNQAIFREAREIDANYITIEAIIIGGEGDVGRCRLKIPPNFVDIDVAITIKLGSS 733  
 QY 645 EKGRDPLSASTIGOPDHNVHLGEGVTKSTPVMTTFEMGSLDSTLRNDGQFTV 704  
 DB 734 EKAKCDPLTEASTINGOPDHNVYILQGVVTRSNPVMITTEYMENGSLDITFLRVNDGKFT 793

QY 705 IOIVGMLRGIAAGKYIADMMYVHRDLAARILVNSLVCKVSPFGSLRELEDDTSPDY 764  
 DB 794 LQILVLMGLIASGYSYLSDDMTVHRDLAARVLYNAOLICKIADPGLSRELEN--ASAY 851  
 QY 765 TSALGKFPFIRMTAPEALIOYRKFTSASDVWSYGIYVMEVMSYGERPYWDMTNOVIA 824  
 DB 852 TTR-GGKIPVMTAPEALIAFRKFTSASDVWSYGYLMEVMSYGERPYWMSNOVIRK 910  
 QY 825 QDYRLPPMDCPSALHQLMDCQKORHRRKFGQIVNTLDKMTIRNPSILKAMPPLSGI 884  
 DB 911 KGYRLPAPMDCPEALYQLMDCQKORHRRKFTSASDVWSYGYLMEVMSYGERPYW 970  
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 AC Q9XZL6;  
 DT 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE EPH TYROSINE KINASE.  
 GN EPH OR CG1511.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophila; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RA He O., Dearborn R., Dai Y., Kunes S.;  
 RT "Drosophila EPH kinase and retinal axon guidance";  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF146648; AAD30170.1; -  
 DR HSSP; P06239; 3LCK.  
 DR Flybase; FBgn0025936; Eph.  
 DR Flybase; FBgn0025936; Eph.  
 DR InterPro; IPR000561; -  
 DR InterPro; IPR000719; -  
 DR InterPro; IPR001090; -  
 DR InterPro; IPR001245; -  
 DR InterPro; IPR001660; -  
 DR InterPro; IPR001777; -  
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 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00336; SAM; 1.  
 DR Pfam; PF01404; EPH\_1bd; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50013; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR SMART; SM00454; SAM; 1.  
 KW ATP-binding; kinase; Tyrosine-protein kinase.  
 SQ SEQUENCE 1035 AA; 116504 MW; EDBE7F1BFED0828 CRC64;

Query Match 39.4%; Score 2017; DB 5; Length 1035;  
 Best Local Similarity 41.5%; Pred. No. 1.8e-144;  
 Matches 442; Conservative 158; Mismatches 310; Indels 146; Gaps 27;  
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 DB 18 LAHADVVLDTTREATLEMTTRPYGQAOTPGWVEESTFDEYKGINW-RSYVCDVAH 76  
 QY 54 SONNMLRTKFIIRRGARHRIHVEKESVROCCSIPVSGCKETFNLYYEADPDSATKTF 113

Db 77 NVNNMLSPFIDRGSANRLYEIQTIRDCSLFPGNALSCKETFSLLFE--FDAATREP 134  
QY 114 PNMENPMVKVDITIADES-FSQ---VDLGRVMKINFEVRSFGVPSRSGFYLAPODYG 169  
Db 135 PMQOTDSYRLIARIAGBGRFNQNSVD-----INTEVKSLA-VNKKGYFAFRDOGA 186  
QY 170 CMSLAVRIFYKRCRIIONGAIPOETLSGAESTSLVAARSGCIANAEEVDPIKLYCNG 229  
Db 187 C1SVLAVKYYITCPAVENFAHFNETPTGREITIIIEKONGCVDNABEPYETPYL-CKG 245  
QY 230 DDEMLVPIGRCMKAGFEAVENGTVCRGCPSTGTFKANOGDEACTHCPINSTRTSSEATNC 289  
Db 246 DGMKTLILGGCKKAGYERNTNKTCTECPLETFKSPYTK-CTPCPPNSNASKTGSPEC 304  
QY 290 VCRNGYRADLDPDMCTTIPSAP-QAVISSVNETSLMLEMTPPRDSG----- 338  
Db 305 KCASGYRHRPNDGRHMPGYPSPAFTNLTLFVDDQTSALISMSAPAKNESFSSETNSKIY 364  
QY 339 REDLYVNIICKSCSGRGACTRCGDNVOYAPROGLTEPRYISDLAHTOYTFEIOAVN 398  
Db 365 HSDIYKTI-----KCNICSPNVVNPSTDTENETKITTLNLEBVTYTVQIHAIN 414  
QY 399 GVTDOSPSPQF-----ASVNITTNQAPSAVS 426  
Db 415 SVSHINEFKRHSNESSLVAVSDIVFSNTSLNIPDLNENKVGQAEIYFTTESVLSTVF 474  
QY 427 IMHOVSRTVDSITLSMSQPDOPNGVILDELOYE-----KELSEYNATAI--KSPNT 478  
Db 475 NDRILATINKADALEMDPVS-----DFPLEYEVGMFPKVELDAINKSALNKETRAH 529  
QY 479 VTGLKAGAIYVOYRARTVAGYRGYSGMYFOTMT--AEYOTSIOEKLPLITGSSAAGL 536  
Db 530 IYGLLENTYEGFOYRCKTNNGFSGYSNMIAQTIQSIVGSYDSDVQ--IRPLAGAIYTV 587  
QY 537 VELLAUVVIAIVCRNGEERADSEYTDKLOHTYSCHI-----TPGMK-- 578  
Db 588 LFLVIFIAIYVEMR-----SKHODLDKSKSTNHLPLPLDYASNEVNSMDTPIVKKL 640  
QY 579 -----IYIDPFYEDPNEAVREFAKEDISCVKIEOVGAGEGEYCSGHLK 625  
Db 641 HLANTTPLFGNSRYVPHYTEEDNCAIREPARIDANVTITIEAIIGGEGDVCRGRK 700  
QY 626 LPGA--REIFVAIKTLKSGYTEKORRDELSEASIMGQFDRPNVILHLEGVYTKSTPVMIIT 683  
Db 701 IPPMFVODIDVAIKTLKPGSSSEKARCDLFEASIMGQFDRPNVILHLEGVYTKSTPVMIIT 760  
QY 684 EFMENGSLOSEFLQONOGFTVIOVGLRGLAIGMKYLADMTVHRDLAARNILVNSNLV 743  
Db 761 EYHENGSLDTFLRNDCKEFTQLIYVLRGLIAGMSYLSMDMNYHRDLAARNILVNAOLI 820  
QY 744 CKVSDFGLSRFLDDTSDPYTSALGKFPRIWTAPEALIOYRKETSASDVWSYGIWMEY 803  
Db 821 CKIADFGLSREIN--ASDAVYTR--GKIPVARTAPEALIAFRKETSASDVWSYGIWMEY 877  
QY 804 MSYGERPYWDMTQODVYINAIEDYRLPPWDCPSALHQLMLDCMKDRNHRPFGQIVNT 863  
Db 878 MSYGERPYWMSQODVIKCEIEKGYRLPAPMDCPEALYQLMLDCWKQRTNRPFAVIST 937  
QY 864 LDKMIRPNSLKAMAPLSSGINPLDRTIPDTSFNTVDENLEAIKMGQYKESFANAGF 923  
Db 938 LONLAPQOSLTLTRPSPESDGNHILDGO--KCONIFISTDLNLEHIKMSRYCHHFEKANL 996  
QY 924 TSFDDVVSQMMMEDILRVGYTLAGHQKILNSIOVMRAQNOIOISV 968  
Db 997 INAQOISRLTAOQLSDMGITLVGHOKKILH-----QARQLDTI 1034

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 24, 2001, 16:29:39 ; Search time 23.96 Seconds

(without alignments)  
2454.310 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 970  
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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 0

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970	100.0	970	16	EPH-like receptor
2	587	60.5	1055	21	Human CASB616
3	480	49.5	987	21	Human CASB616
4	322	33.2	994	16	Receptor tyrosine
5	322	33.2	994	18	Mouse Nuk tyrosine
6	103	10.6	995	16	EPH-related PTK Ce
7	103	10.6	1011	16	EPH-related PTK Ce
8	77	7.9	77	21	Mouse ephrin B rec
9	40	4.1	998	16	EPH-like receptor
10	40	4.1	998	17	Mouse developmenta
11	39	4.0	59	14	Partial bptkl gene

12	39	4.0	59	16	AA85924
13	37	3.8	57	16	AA79141
14	37	3.8	57	19	AAW79147
15	37	3.8	57	20	AAW81404
16	36	3.7	973	16	AAW75707
17	35	3.6	988	16	AAW75708
18	35	3.6	988	16	AAW75710
19	35	3.6	990	15	AAW51899
20	35	3.6	993	16	AAW75843
21	35	3.6	993	16	AAW75844
22	32	3.3	951	16	AAW75704
23	31	3.2	260	16	AAW76467
24	31	3.2	380	14	AAW44512
25	31	3.2	849	16	AAW75706
26	31	3.2	972	16	AAW76468
27	31	3.2	972	17	AAW06531
28	31	3.2	984	14	AAW44513
29	31	3.2	986	16	AAW85936
30	31	3.2	986	16	AAW85091
31	31	3.2	987	16	AAW85091
32	31	3.2	987	16	AAW85930
33	31	3.2	987	17	AAW06535
34	31	3.2	987	17	AAW94652
35	31	3.2	987	18	AAW13304
36	31	3.2	1293	14	AAW41896
37	29	3.0	40	16	AAW85097
38	28	2.9	710	16	AAW75714
39	28	2.9	722	16	AAW75705
40	28	2.9	744	16	AAW75713
41	28	2.9	948	20	AAW83148
42	24	2.5	57	19	AAW79148
43	24	2.5	57	20	AAW81405
44	24	2.5	877	19	AAW71628
45	24	2.5	928	17	AAW97853

#### ALIGNMENTS

RESULT	1
AA85089	AA85089 standard; Protein; 970 AA.
ID	AA85089
AC	AA85089;
XX	16-APR-1996 (first entry)
DT	EPH-like receptor protein tyrosine kinase HEK5.
XX	EPH-like receptor protein tyrosine kinase; PTK; HEK5;
XX	human eph-like kinase; therapy; diagnosis; vector; antibody.
OS	Homo sapiens.
XX	W09528484-A1.
PN	26-OCT-1995.
PD	14-APR-1995; 95WO-US04681.
XX	15-APR-1994; 94US-0229509.
PR	(AMGE-) AMGEN INC.
PA	Fox GM, Jing S, Welcher AA;
XX	WPI: 1995-373799/48.
XX	N-PSDB; AAT02946.
DR	New nucleic acid encoding EPH-like receptor tyrosine kinase(s)
PT	and related vectors, host cells, proteins, antibodies etc., used
PT	diagnostically and therapeutically to modulate receptor activation
PT	or prodn.

Protein tyrosine-k  
Human receptor typ  
Receptor protein t  
Receptor protein t  
Eph-related PTK Ce  
Eph-related PTK Ce  
Eph-related PTK Ce  
Human embryonal ki  
Protein p140 CDNA  
Protein p140 CDNA  
Eph-related CEK6.  
Non-differentiated  
Elk PTK, Rattus r  
Eph-related PTK Ce  
Mature non-differe  
Full-length recept  
alk. Rattus ratu  
Protein tyrosine-k  
EPH-like receptor  
Human non-differen  
Protein tyrosine-k  
Full length recept  
Receptor type tyro  
Receptor-type tyro  
PTK gene Hprt5 pro  
EPH-like receptor  
Eph-related PTK Ce  
Eph-related PTK Ce  
Eph-related PTK Ce  
Receptor protein t  
Receptor protein t  
Mouse Bsk receptor  
Rat Rck7 eph-relat

XX Claim 18; Page 46-49; 133pp; English.

PS 4 Novel human Eph-like receptor protein tyrosine kinases, HEK5, HEK7,  
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following  
 CC isolation of their encoding cDNAs (AA02946-49) from a human fetal  
 CC brain cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the  
 CC catalytic domain of chicken Eph-like receptors Cerk, Cerk7 and Cerk8.  
 CC HEK11 shows no homology to any known Eph-like receptor. Recombinant  
 CC HEK1 receptors (or their soluble extracellular domains) are produced by  
 CC expression of encoding sequences in prokaryotic or eucaryotic host  
 CC cells, and are used to produce antibodies (utilised in diagnostic  
 CC assays), or to identify and purify ligands for HEK receptors, or  
 CC therapeutically to modulate the activation of cell-associated  
 CC receptors. Soluble HEK5 receptor may affect primarily brain and  
 CC pancreatic cells.

XX Sequence 970 AA:

SO Query Match 100.0%; Score 970; DB 16; Length 970;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAARETLMDSTTATAEELGMVHPSPGMEVSGYDENMNTIRTYOCNVFESSQNNMLR 60  
 DB 1 llaaveelmdstataelgymwvhpssgweevsgydenmnlrttyocnvfessqnnwlr 60  
 QY 61 TKFIRRGARHRIHVEKMFVSDCSSIPVPGSKETFNLYYADPDSATKTFPPNMENP 120  
 DB 61 tkfirrgarhrihvekmfvsdcssipvpgsketfnlyyadpdsatktpfnmemp 120  
 QY 121 WVVVDRTAADESPQVLDGRVVKINTEVRSFGVRSRGYFLAFQYGGCMSLIAVRFV 180  
 DB 121 wvvvdrtaaadespqvldgrvvkintevrsfgvrsrgyflafqyggcmsliaavrfv 180  
 QY 181 RKCPRIIONAIFOETLSGAESTSLVARGSCIANAEVDVPIKLCNCGDGEMLVPIGR 240  
 DB 181 rkcpriionaifoetlsgaestslvargscianaevdvpiklcnngdgemlvpigr 240  
 QY 241 MCKRAGFAVENGYKRCGPGSTGRKANGDACHHCPINSTTSEGANCYCRNGYRADL 300  
 DB 241 mckragfavengykrccpgstgrkangdachhccpinsttsegancycrnyradl 300  
 QY 301 DPLDMPCTTIPSAFOAVISSVNETSLMLEWTPPRDSGREDIVNIICKSCSGRGAC 360  
 DB 301 dpldmpcttipsafavissvnetslmlewtpprdsgrredivniickscsgrgac 360  
 QY 361 CGDNVOYAPRQLGLTEPRIRYISDLAHTOYTFETIQAVNVGTDSFSPQFASVNTT 420  
 DB 361 cgdnvoyaprqlglteprirysdlahytoytfetiqaavnvgtdsfspqfasvntt 420  
 QY 421 APSAVSITMHOVSRVDSITLWSQPDQPNVILIDYEOYKEKELSEVNATAISPT 480  
 DB 421 apsavsitmhovsrvdsltlwsqpdqpnvildyeyokekelsenvataispt 480  
 QY 481 GLKGAIFYEFOVRATYAGRGYSGKMYFOTMTEAEYOTSIOEKLPIIICSSAG 540  
 DB 481 glkgaiyfeovratyagrgysgkmyfotmteaeeyotsioeklpiiicssag 540  
 QY 541 AVVIAIAVNCNRGFERADSEYTDKLQHTYSGHTPGMKIYIDPPTYDDPDNAVRE 600  
 DB 541 avviaiaavncnrgferadseytdklqhtysghtpgmkiyidpptyddpdnavre 600  
 QY 601 DISCVKIEQVIGAGEFEGVSCGHLKPGKREIFAITIKISGVEKORPFLSAS 660  
 DB 601 discvkieqvigagefegvscghlpgkreifaitikisgvekorpflsas 660  
 QY 661 FDHNVAHLEGVTKSTPVMIITEFMENGSLDSFLRQNDGQFVTLQVGMRLGIA 720  
 DB 661 fdhnvahlegvtkstpvmiitefmengslldsflrqndgqfvtlqvgmrlgia 720  
 QY 721 LADNMVYHRDLAARNILVNSMLVCVSDPGLSRFLDDTSDPYTTSALGCKFP 780

DB 721 ladnmvyhrdlaarnilvnsmlvcvsdpglsrflddtspytsalgcgkfp 780

QY 781 ALOYRKFTSASDVMSYGIWMEVMSYGERPPTMDTNDYINAIEDVRLRPPMDCPS 840  
 DB 781 aloyrkftsasdvmsygiwmevmsygerpptymdtndyinaiedvrlrppmdcps 840

QY 841 QIMLDCWKDRHRKPGQIVYTLTKMIRNPNSLKAMAPLSGILPLDRTIPDYTSFN 900  
 DB 841 qimldcwkdrhrkpgqivytltkmirnpnslkamaplsgilpldrtipytsfn 900

QY 901 TYDEMLEAIKMOYKESFANAGTSPDYVSQMMEDILRVGYTLAGHOKILNSIQ 960  
 DB 901 tydeMLEAIKmqykesfanagtsfdvvsqmmmedilrvgytlaghqkllnsiq 960

QY 961 QMNQIQSVYEV 970  
 DB 961 qmnqisvsev 970

RESULT 2  
 AAB19591  
 ID AAB19591 standard; Protein: 1055 AA.  
 XX AAB19591;  
 XX 22-JAN-2001 (first entry)  
 DE Human CASB616.  
 XX CASB616; EPHB2; ERK; EPH3; EPH3T3; DRT; HEK5; EPHB2V;  
 KW receptor protein tyrosine kinase; human; antigen; colon cancer;  
 KW ovary cancer; autoimmune disease; vaccine; therapy; diagnosis.  
 XX Homo sapiens.  
 OS WO200003216-A2.  
 PN 14-SEP-2000.  
 PD 28-FEB-2000; 2000WO-IP01587.  
 PF 05-MAR-1999; 99GB-0005124.  
 PR (SMK) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA Vinals De Bassols VC.  
 PI WPI: 2000-587384/55.  
 DR N-PSDB: AAA88549.  
 DR Vaccine composition for treating ovarian and colon cancer, comprises  
 PT CASB616 polypeptides, polynucleotides or antigen presenting cells  
 PT expressing the polypeptides -  
 PS Claim 1; Page 42; 57pp; English.

XX The present sequence is that of human CASB616, a member of the Eph  
 CC and Eph-related family of receptor protein tyrosine kinases.  
 CC CASB616 is also known as EPHB2, ERK, EPH3, EPH3T3, DRT, HEK5 and  
 CC EPHB2V. CASB616 polypeptides and polynucleotides are important  
 CC immunogens for specific prophylactic or therapeutic immunization  
 CC against tumours, especially colon cancer (claimed) and ovarian  
 CC cancer. They are specifically expressed or highly over-expressed  
 CC in tumours compared to normal cells and can thus be targeted by  
 CC antigen-specific immune mechanisms leading to destruction of the  
 CC tumour cells. They can also be used to diagnose the occurrence of  
 CC induction of autoimmune responses, which can be corrected through  
 CC vaccination using the CASB616 polypeptides or polynucleotides.

SO Sequence 1055 AA:

Query Match 60.5%; Score 587; DB 21; Length 1055;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 967; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

1 LLAAVEETLMDSTTATAELGMVHPPSGWEVSGYDENMNTIRTYQVCNVESSQNMMLR 60  
15 llaaveetlmdstataelgmvhppsgwevsgydenmnlrtlygvcnvfessqnmvlr 74  
61 TKFIRRRGAHRIHVEKFEFVRDCSSIPSPGSCKEFNLYYYEADPDSATKTFPMWMMNP 120  
75 tkfirtgrghrihvenkfefvrcdssipspgsketfnlyyyeadpdsatktfpmwmp 134  
121 WKVVDTLADESFOYDLGGRVWKINTEVRSFGVSRSGFYLAFODYGGCSMLIAVRVY 180  
135 wkvvdtdlaadesfagvdyldgrvwmkintevrsfgvrsrsgfyiafdyggscmsllavrvly 194  
181 RKCPRITONGAIFOEFTLSGAESTSLVAARGSCIANAEVDPAIKIXCGDGEMLVPIORC 240  
195 rkcpitlmgafifgecltgaestsivaargscianaeevdpaikilycngdgewlvpiqrc 254  
241 MCKAGPEAVENGTCVRCGPGSTFKANQGDDEACTHCPINSRTTSECATNCVCRNGYRADL 300  
255 mckagfeavengtcvrcgpgstfkanggddeacthpcnrttsesgactncvcrnyradl 314  
301 DPLDMPCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVNIIICKSCGSGRGACTR 360  
315 dpldmpcttipapqavissvnetslmewtpprdsgrredlvyniickscsgsrgactr 374  
361 CGDNVQVAPROGLTEPRITVYISDLAHTQYTFEIOAVNGVVDOSFSPQFASVNTINNOA 420  
375 cgdnvqyaprgltleprilytsdlahthqytfelgavngvddgspfqfssvnltnqga 434  
421 APSAISMHOVSRYVDSTTILSMQDPDNGVILDELOYEKELSEKNATAIKSPNTVT 480  
435 apsaismhqvsvryvdstiltlsmqdpdngvildeloyekelseyknataikspntvt 494  
481 --GLKAGAIYFQVAVARVAGYGRSGKMFQMTAEVQSTOEKPLRITIGSSAAGLVF 538  
495 vglkagailvyfqrarvavagyrsgkmyqumtlaeyqstlqeklplligssaaglvf 554  
539 LIAVVVIAIVCNRRGFERADSEYTDKLOHTYSGHITPQMKIYIDPTVEDPNEAVREFAK 598  
555 liavvvialvncnrrgferadseytldklohtysshitpqmkiyidptvedpneavrefak 614  
599 EIDISCVYIEOVIGAGEGVCSCGHLKLPKRELFVAIKTLKSYTEKORRDLSEASIM 658  
615 eidiscvkievigaagegvcsghlklpkrelfvaiktlksytekordlfsseasim 674  
659 GQFDHPNVILHEGVYTKSTPVMITTEFMENGSLDSFLRONDGQFTVITQLVGMRLGIAAGM 718  
675 gqfdhpnvilhgyvtykstpvmittetfemengslsdlrondgqftvltqlvgmlrgiaagm 734  
719 KYLADMYVHNDLAAARNILVNSNLVCVSPFGASRFLIEDTSDPTTYTSAUGKFPRIWTA 778  
735 kyladmyvhtdlaarnilvnsnlvcvspfsgasrfliedtspdytsaigkfpriwta 794  
779 PEALQYRKFTSASDVMSTGYIVMEVNSYGERPYWDMTNOVINAIEDDYVLPMPMCCPSA 838  
795 pealqyrkftsasdvmsygyivmewnsygerpywdmtngvlnaieddyvlpmpmccpsa 854  
839 LHQMLDCKOKDRNHRPKFCQIYVNTLDKMTIRNPNSIKAMAPLSSGSLNPLLDRTTIPDYTS 898  
855 lhqmldcwkdkdrnhpkfcqiyvntldkmtirnpnsikamaplsnplldrttipdyts 914  
899 FNTYDVELEAIKKGQVRESFANAGFTSFDVVSQMMEDILRVGVTLAGHOKKTLNSIQVA 958  
915 fntydeleaikgqvresfanagfsvdvvsqmmmedilrvgvtaghokktilnsiqvm 974  
959 RAQMNOIQSVE 969  
975 raqmnoiqsve 985

RESULT 3  
AAB19590  
ID AAB19590 standard; Protein: 987 AA.  
XX  
AC AAB19590;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Human CASB616.  
XX  
KW CASB616; EPHB2; ERK; EPH3; EPH73; DR7; HEK5; EPHB2v;  
KW receptor protein tyrosine kinase; human; antigen; colon cancer;  
KW ovary cancer; tumour; autoimmune disease; vaccine; therapy;  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 568..569  
FT /note="an additional Arg residue decodes from the  
FT CASB616 nucleotide sequence given in the  
FT specification (see AAB8548), but is not  
FT given in the CASB616 amino acid sequence in  
FT the specification"  
FT Misc-difference 956  
FT /note="encoded by GTR"  
FT  
PN WO200053216-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 28-FEB-2000; 2000WO-BP01587.  
XX  
PR 05-MAR-1999; 99GB-0005124.  
XX  
PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Vinals De Bassols YC;  
XX  
DR WPI: 2000-587384/55.  
DR N-PSDB: AAB8548.  
XX  
PT Vaccine composition for treating ovarian and colon cancer, comprises  
PT CASB616 polypeptides, polynucleotides or antigen presenting cells  
PT expressing the polypeptides  
XX  
PS Claim 1: Page 41; 57pp; English.  
XX  
CC The present sequence is that of human CASB616, a member of the EPH  
CC and EPH-related family of receptor protein tyrosine kinases.  
CC CASB616 is also known as EPHB2, ERK, EPH3, EPH73, DR7, HEK5 and  
CC EPHB2v. CASB616 polypeptides and polynucleotides are important  
CC immunogens for specific prophylactic or therapeutic immunization  
CC against tumours, especially colon cancer (claimed) and ovarian  
CC cancer. They are specifically expressed or highly over-expressed  
CC in tumours compared to normal cells and can thus be targeted by  
CC antigen-specific immune mechanisms leading to destruction of the  
CC tumour cells. They can also be used to diagnose the occurrence of  
CC tumour cells. Their inappropriate expression can also cause an  
CC induction of autoimmune responses, which can be corrected through  
CC vaccination using the CASB616 polypeptides or polynucleotides.  
XX  
SQ Sequence 987 AA;  
XX

Query Match 49.5%; Score 480; DB 21; Length 987;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LLAAVEETLMDSTTATAELGMVHPPSGWEVSGYDENMNTIRTYQVCNVESSQNMMLR 60  
15 llaaveetlmdstataelgmvhppsgwevsgydenmnlrtlygvcnvfessqnmvlr 74

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OY 61 TKPIRRGAHRIHVEKKEPSVRDCSSIPVSGCKETFNLYYEADFDSATKTFPMNMENP 120
DB 75 LKILIRGAHRIHVEKKEPSVRDCSSIPVSGCKETFNLYYEADFDSATKTFPMNMENP 134
OY 121 WVKVDPIADSEFSOVDLGGRWKINTFEVRSFGPVSRSGFYLAFOYGGCMLIAVRFFY 180
DB 135 WVKVDIAADESFISQVDLIGRWKINTFEVRSFGPVSRSGFYLAFOYGGCMLIAVRFFY 194
OY 181 RKCPRIIOGAIKQETLSGAESSTVAARGSCIANEEDVPIKLYCNGDEMLVPIGRC 240
DB 195 RKCPRIIOGAIKQETLSGAESSTVAARGSCIANEEDVPIKLYCNGDEMLVPIGRC 254
OY 241 MCKAGFEAVENGTVCRGCGSGTFKANKQGDGACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 255 mckagfeavengtvcrpgsggttkanggdeacthcpinsrttsegatncvcrngyradl 314
OY 301 DPIDMECTTTPSAPOAVISSVNTSITMLEWTPPRDSGREDLYNITICKSGSGRGACTR 360
DB 315 dpidmectttsapqavissvntslmlewtpprdsqgredlynllicksgsgrgactr 374
OY 361 CGDNVOYAPRQLGTFEPRITISDLAHTQYTFEIOAVNGVTDOSPPSPQFASVNTTNOA 420
DB 375 cgdnvgyaprqglteprityisdlahtqytfelqavngvtdosppsfasvntltnga 434
OY 421 APSAVSIMHOVSRTVDSITLWSQPDOPNGVITLDYELQYTERKELSEYNATAIKSPNTVT 480
DB 435 apsavsimhovsrtvdsitlwsqpdopngvitldyelyekelseynatalakspntvt 494

```

## RESULT 4

AAR87018 standard; Protein; 994 AA.

AAR87018:

19-MAR-1996 (first entry)

Receptor tyrosine kinase (neural kinase).

Receptor tyrosine kinase; neural kinase; Nuk; axon;

axogenesis; nerve disorder.

Mus musculus.

Location/Qualifiers

1..26 /label= Sig\_peptide

27..548 /label= Extracellular region

/note= "the extracellular region (amino acids 27-548) includes an N-terminal Ig-like domain and an Ig-like Nuk repeat"

330..420 /label= FNIII

/note= "fibronectin type III repeat"

444..534 /label= FNIII

/note= "fibronectin type III repeat"

549..574 /label= Transmembrane\_region

575..994 /label= Cytoplasmic\_region

623..707 /label= Tyrosine\_kinase\_catalytic\_domain

W09530326-A1.  
09-NOV-1995.  
28-APR-1995; 95WO-CA00254.  
29-APR-1994; 94US-0235407.

```

XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
PA Henkemeyer M, Letwin K, Pawson A;
PI WPI: 1995-393299/50.
XX N-PSDB: AAT07308.
DR
PT DNA encoding neural receptor tyrosine kinase - useful in gene
PT therapy of nerve disorders, and for diagnosis and identification of
PT therapeutic agents
PS Claim 1, Page 70-74; 103pp; English.
XX
XX A novel receptor tyrosine kinase (AAR87018), designated neural kinase
CC (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obtd. from a mouse
CC embryo library. Nuk is expressed in migrating axons and is
CC involved in cell-cell interactions and axogenesis in development
CC of the nervous system. Nuk or its fragments (pref. amino acids
CC 26-548 or 601-994) are used to identify (ant)agonists of the
CC (activated) receptor tyrosine kinase as a means of treating nerve
CC disorders and damage, or to raise antibodies used to monitor axon
CC migration and nerve cell interactions.
SQ Sequence 994 AA:

```

Query Match 33.2%; Score 322; DB 16; Length 994;

Best Local Similarity 100.0%; Pred. No. 0; Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 159 GFYLAFODYGGCMLIAVRVFRKCPRIIOGAIKQETLSGAESSTVAARGSCIANEE 218
DB 181 gfylafdyggcmliavrvfyrkcpriiogaikqetlsgaestsivaargsciaanee 240
OY 219 VDVPIKLYCNGGEMVPIGRMCKAGFEAVENGTVCRGCGSGTFKANKQGDGACTHCPIN 278
DB 241 vdvpiiklycnggemvpiigrmckagfeavengtvcrpgsggttkanggdeacthcpin 300
OY 279 SRTSEGATNCVCRNGYRADLPIIDMECTTTPSAPOAVISSVNTSITMLEWTPPRDSG 338
DB 301 srtsegatncvcrngyradlpidmectttsapqavissvntslmlewtpprdsdg 360
OY 339 REDLVNITICKSGSGRGACTRCGDNVOYAPRQLGTFEPRITISDLAHTQYTFEIOAVN 398
DB 361 redlvniticksgsgrgactrcgdnvgyaprqglteprityisdlahtqytfelqavn 420
OY 399 GVTDOSPEFSPOFASVNIITNOAAPSASVIMHOVSRTVDSITLWSQPDOPNGVITLDYELQ 458
DB 421 gvtDOSPEFSPOFASVNIITNOAAPSASVIMHOVSRTVDSITLWSQPDOPNGVITLDYELQ 480
OY 459 YVEKELSEYNATAIKSPNTVT 480
DB 481 yvekelseyatalakspntvt 502

```

## RESULT 5

AAW26366 standard; Protein; 994 AA.

AAW26366:

02-DEC-1997 (first entry)

Mouse Nuk tyrosine kinase.

Nuk tyrosine kinase; Eph receptor tyrosine kinase;

signal transduction; axonogenesis; neurodegenerative disease;

Alzheimer's disease; Parkinson's disease; Huntington's disease;

multiple sclerosis; amyotrophic lateral sclerosis;

Wernicke's disease; nerve damage; trauma; ischaemia; stroke.

Mus musculus.

XX Key Location/Qualifiers  
 FH Peptide 1..26  
 FT /label= Sig-peptide  
 FT 27..994  
 FT Protein /label= Mat-protein  
 FT Domain 27..348  
 FT /label= Extracellular\_domain  
 FT Region 330..420  
 FT /label= FNIII  
 FT /note= "fibronectin type III repeat"  
 FT 444..534  
 FT /label= FNIII  
 FT /note= "fibronectin type III repeat"  
 FT 549..574  
 FT /label= Transmembrane\_domain  
 FT 575..994  
 FT /label= Cytoplasmic\_domain  
 FT 623..888  
 FT /label= Tyrosine-kinase\_region  
 FT  
 PN W09714966-A1.  
 PD 24-Apr-1997.  
 PE 10-OCT-1996; 96WO-CA00679.  
 PR 13-OCT-1995; 95US-0005518.  
 PA (MOUNT SINAI HOSPITAL CORP.  
 PI Henkemeyer M, Dawson A;  
 DR WPI: 1997-245245/22.  
 DR N-PSDB: AAT84528.  
 XX  
 PT Activation of ligand regulatory pathways by Eph subfamily receptor  
 PT tyrosine kinases - for stimulating or inhibiting axonogenesis,  
 PT useful for treatment of e.g. neurodegenerative diseases such as  
 PT Alzheimer's or Parkinson's diseases  
 PS Disclosure; Fig 3; 55pp; English.  
 XX  
 CC Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine  
 CC kinase that is essential for formation of the medial tract of the  
 CC anterior commissure of the brain, and which appears to play a  
 CC role in the formation of the habenular interuncle tract. Its  
 CC amino acid sequence was deduced from cDNA clones (see AAT84528).  
 CC Isolated from an embryo cDNA library. The extracellular domain  
 CC of Nuk was shown to be sufficient for formation of the medial  
 CC tract. Eph subfamily receptor tyrosine kinases (e.g. the Nuk  
 CC extracellular domain) can be used in claimed methods to: activate  
 CC a ligand regulatory pathway in a cell; identify substances able to  
 CC bind a ligand for an Eph subfamily receptor tyrosine kinase; and  
 CC to affect neuronal development or regeneration, especially the  
 CC stimulation or inhibition of axonogenesis, in a mammal. Activation  
 CC of the ligand regulatory pathway results in downstream activation  
 CC of a series of regulatory pathways in cells that control gene  
 CC expression, cell division, cytoskeletal architecture, cell  
 CC metabolism, cell migration and cell-cell interactions. Substances  
 CC which activate the ligand regulatory pathway may be used for  
 CC stimulating or inhibiting neuronal development regeneration and  
 CC axonal migration associated with neurodegenerative disease e.g.  
 CC Alzheimer's, Parkinson's or Huntington's diseases, multiple  
 CC sclerosis, amyotrophic lateral sclerosis, deficiency diseases such  
 CC as Mernicke's disease, peripheral nerve damage, trauma and  
 CC ischemia resulting from stroke.  
 XX  
 XX Sequence 994 AA:

Query Match 33.2%; Score 322; DB 18; Length 994;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 159 GFTYAFODYGGCMLIVAVRYRKCPRIONGAIPEFTLSGAESTSLVAARGSCIANAE 218  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 gftlafqdyggcmalavrvlyrkcprihqalifgelisgaestsavaarqscianae 240  
 QY 219 VDVPDKLYCNGDGEMLVPIGRMCKAGEAVENTVCNGCSTGTFKANOGDEACTHGPIN 278  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 vdvpikllycngdgewlvpigrcmekagfeavengtvrcpsgfkanggeacthpin 300  
 QY 279 SRTTSEATNCVNCNGYRRALDPLDPCTTTPAPQAVISVNETSLMLEWTPRRSGG 338  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 srttseatncvcnngyrradlpldpcttispapavissvnetslmlewtprds9g 360  
 QY 339 REDLVYNIICKSCSGRGACTRCGDNVQYAPROLGTEPRYISDLAHTQYFEIOAVN 398  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 redlvynlickscsgsgyactrcgdnvqyaprglgeprlyisdllahncylteiqavn 420  
 QY 399 GVTDSPPSPQFASVNTTNOAPSAVSIMHVSRTVDSITLSWSQDPDNGVILDYELQ 458  
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 gvtqspfpqfasvntltngapavsimbqvarvtvdsitlswsqdpdngvildyql 480  
 QY 459 YYEKELSEYNATAIKSPNTVT 480  
 Db ||||||||||||||||||||||||||||  
 Db 481 yyekealseynataikspntvt 502  
 RESULT 6  
 AAR75712  
 ID AAR75712 standard; Protein: 995 AA.  
 XX  
 AC AAR75712;  
 XX  
 DT 11-NOV-1995 (first entry)  
 XX  
 DE Eph-related PTK Cdk5.  
 XX  
 KW Cdk5; Eph: protein tyrosine-kinase; PTK; cancer; diagnosis;  
 KM prognosis.  
 XX  
 OS Gallus sp.  
 XX  
 PN W09515375-A.  
 PD 08-JUN-1995.  
 PF 07-SEP-1994; 94WO-US10140.  
 PR 03-DEC-1993; 93US-0162809.  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 PI Pasquale EB, Sajjadi FG;  
 DR WPI: 1995-215256/28.  
 DR N-PSDB: AAQ90660.  
 PT Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
 PT cancer.  
 PS Disclosure; Page 92-96; 129pp; English.  
 XX  
 CC Probes derived from the EPH-related PTKs Cdk4 (AAQ90659) and Cdk5  
 CC (AAQ90660) were used to isolate novel cDNA clones (AAQ90652-58,  
 CC AAQ90661-62) from chicken embryo and embryonic brain libraries.  
 XX  
 XX Sequence 995 AA:

Query Match 10.6%; Score 103; DB 16; Length 995;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 574 TPGMKIYIDPFTYEDNEAVREFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPGRKEIF 633
   |||||||
Db 599 tpgmklyidpftyeopneavrefakeidiscvkieqyigagefgevcshlkilpgkreif 658
OY 634 VAIKTIKSGYTERKORDFLSEASIMGQFDPHPNYIHLEGVVTKS 676
   |||||||
Db 659 valktiksgytekqrdrflseasimgqfdpnpvihlegvvtks 701

RESULT 7
AAR75709
ID AAR75709 standard; Protein; 1011 AA.
XX
XX AAR75709;
AC
XX 11-NOV-1995 (first entry)
DT
XX Eph-related PTK Cdk5+.
DE
XX Cdk5+: Eph; protein tyrosine-kinase; PTK; cancer; diagnosis;
KM prognosis.
XX Gallus sp.
OS
XX WO9515375-A.
XX
XX 08-JUN-1995.
PD
XX 07-SEP-1994; 94MO-US10140.
PF
XX 03-DEC-1993; 93US-0162809.
PR
XX (LJOL-) LA JOLLA CANCER RES FOUND.
PA
XX Pasquale EB, Sajjadi FG;
PI
XX WPI: 1995-215256/28.
DR
XX N-PSDB; AAQ90657.
XX
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
PT cancer.
XX
XX Claim 11; Page 71-75; 129pp; English.
XX
XX A cDNA clone encoding a novel variant of Eph-related PTK Cdk5,
CC Cdk5+ (AAQ90657), was isolated from a chick embryo library in
CC lambda gt11. Cdk5+ protein (AAR75709) contains a 16-amino acid
CC insertion in the juxtamembrane domain, and be a result of
CC alternative splicing. Cdk5+ is exclusively expressed in the CNS.
XX
XX Sequence 1011 AA;

Query Match 10.6%; Score 103; DB 16; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.2e-100; Indels 0; Gaps 0;
Matches 103; Conservative 0; Mismatches 0;

OY 574 TPGMKIYIDPFTYEDNEAVREFAKEIDISCVKIEOVIGAGEFGEVCSGHLKLPGRKEIF 633
   |||||||
Db 615 tpgmklyidpftyeopneavrefakeidiscvkieqyigagefgevcshlkilpgkreif 674
OY 634 VAIKTIKSGYTERKORDFLSEASIMGQFDPHPNYIHLEGVVTKS 676
   |||||||
Db 675 valktiksgytekqrdrflseasimgqfdpnpvihlegvvtks 717

RESULT 8
AAB14401
ID AAB14401 standard; Protein; 77 AA.
XX
XX AAB14401;
AC
XX 14-NOV-2000 (first entry)
DT

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XX
DE Mouse ephrin B receptor EphB2 sterile alpha motif (SAM) domain.
XX
XX SAM domain; sterile alpha motif; homodimerisation; heterodimerisation;
XX signal transduction; X-ray crystallography; protein coordinate data;
XX drug development; antibody; T-cell signalling; telomere function;
XX cell proliferative disorder; senescence; ageing; cancer; atherosclerosis;
XX arthritis; angiogenesis; neuronal development; axonal migration;
XX neurodegeneration; neurodegenerative disease; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; demyelinating disease;
XX multiple sclerosis; amyotrophic lateral sclerosis; nervous system trauma;
XX stroke; ischaemia; cytoskeletal; immunosuppressive; vulnerability;
XX neuroprotective; nocrotropic; antiparkinsonian; cerebroprotective;
XX antiarthritic; antiatherosclerotic; EphB2; ephrin B receptor; murine;
XX receptor tyrosine kinase; mouse.
XX
XX Mus musculus.
OS
XX
XX WO200037500-A1.
XX
XX 29-JUN-2000.
PD
XX 17-DEC-1999; 99MO-CA01209.
PF
XX 18-DEC-1998; 98US-0112929.
PR
XX (MOUN ) MOUNT SINAI HOSPITAL.
PA
XX Stapleton D, Sichert F;
PI
XX WPI: 2000-442645/38.
DR
XX
XX 3-D structure of sterile alpha motif domain used as model for
PT determining 3-D structures of additional native or mutated SAM domain
PT with unknown structure and structures of co-crystals of SAM domain with
PT modulators.
XX
XX Disclosure; Page 60; 72pp; English.
XX
XX The invention relates to the three dimensional structure of a SAM
CC (sterile alpha motif) domain, to peptides (AAB14420-B14525) which mediate
CC SAM domain function, and to potential modulators of SAM domain function.
CC The SAM domain mediates homo- and heterodimerisation and is found in cell
CC surface receptors, cytoplasmic signalling proteins, transcriptional
CC activators and repressors and chimeric human oncoproteins. For example it
CC is present in the Eph family of receptor tyrosine kinases, the
CC transcription factor TEL, members of the polycarb group of
CC transcriptional repressors (e.g., RAR28, Scm), the protein kinase Bcrp
CC and Liprin scaffolding proteins. SAM domains are therefore thought to
CC play an important role in both normal and oncogenic signal transduction.
CC The X-ray crystal structure was determined for the SAM domain of the
CC murine ephrin A receptor isoform EphA4 (AAB14400; also known as Sek,
CC Sek1, Cdk8, Hek8, and Tyro1). The SAM domain corresponds to residues
CC 890-981 of EphA4. The 3D structure of the SAM domain can be used in the
CC determination of the structures of other SAM domain-containing proteins.
CC The SAM domain peptides may be used to identify compounds for drug
CC development and to prepare antibodies. The antibodies can be used to
CC screen for SAM domain-containing proteins, to diagnose and treat
CC disorders associated with aberrant T-cell signalling, and to modulate
CC telomere function. Modulators of SAM domain function may be used to treat
CC diseases associated with inappropriate activity of a protein containing a
CC SAM domain, particularly an Eph receptor. They may be used to treat a
CC cell proliferative disorder such as cancer, atherosclerosis, arthritis
CC and diseases associated with the nervous system, and may be used to
CC modulate angiogenesis. The SAM domain peptides and modulators may be used
CC to modulate the biological activity of an Eph receptor or Eph ligand in a
CC cell, particularly in pathways involved in neuronal development, axonal
CC migration, pathfinding and regeneration. Compositions containing SAM
CC domain modulators may be used in the treatment of neurodegenerative
CC diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, demyelinating diseases such as multiple sclerosis, and
CC amyotrophic lateral sclerosis) and conditions involving trauma and injury
CC to the nervous system (e.g., ischaemia resulting from stroke, and

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CC bacterial and viral infection of the nervous system). The present  
 CC sequence represents the SAM domain of murine EphA2.  
 XX

SO Sequence 77 AA:

Query Match 7.9%; Score 77; DB 21; Length 77;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-74;  
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 894 PDYTSFNTVDEMLFAIKKGOYKESFANAGTSPDVVSQMMEDILRVGVTLAGHQKILN 953  
 |||  
 Db 1 pdytsfntvdeleakmgqkfstanagtsfdvsgmmmedilrvyvtlaghqkkin 60  
 |||  
 OY 954 SIQVWRAQMNQIQSYEV 970  
 |||  
 Db 61 siqvmraqmqiqsyev 77

RESULT 9  
 AAR85092  
 ID AAR85092 standard; Protein: 998 AA.

AC AAR85092;

DT 16-APR-1996 (first entry)

DE EPH-like receptor protein tyrosine kinase HEK11.

KM EPH-like receptor protein tyrosine kinase; PTK; HEK11;

KW human eph-like kinase; therapy: diagnosis; antibody; vector.

OS Homo sapiens.

PN WO9528484-A1.

PD 26-OCT-1995.

PF 14-APR-1995; 95WO-US04681.

PR 15-APR-1994; 94US-0229509.

PA (AMGE-) AMGEN INC.

PI Fox GM, Jing S, Welcher AA;

DR MPI; 1995-37379/48.

DR N-PSDB; AAT02949.

PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) -  
 and related vectors, host cells, proteins, antibodies etc., used  
 PT diagnostically and therapeutically to modulate receptor activation  
 or prodn.

PS Claim 18; Page 71-75; 133pp; English.

CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,  
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following  
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal  
 CC brain cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the  
 CC catalytic domain of chicken EPH-like receptors Cck5, Cck7 and Cck8.  
 CC HEK11 shows no homology to any known EPH-like receptor. Recombinant  
 CC HEK receptors (or their soluble extracellular domains) are produced by  
 CC expression of encoding sequences in prokaryotic or eucaryotic host  
 CC cells, and are used to produce antibodies (utilised in diagnostic  
 CC assays), or to identify and purify ligands for HEK receptors, or  
 CC therapeutically to modulate the activation of cell-associated  
 CC receptors.

SO Sequence 998 AA:

Query Match 4.1%; Score 40; DB 16; Length 998;

Best Local Similarity 100.0%; Pred. No. 2.3e-33;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RWTAPDAIQKFTSADVWSTGIVMEVMSYGERPYWDM 814  
 |||  
 Db 801 rwtapeaiqykftsaadvswsgivmewmsysgerpywdm 840  
 |||

RESULT 10

AAR03421  
 ID AAR03421 standard; Protein: 998 AA.

AC AAR03421;

DT 11-NOV-1996 (first entry)

DE Mouse developmental kinase 1.

KM Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;  
 KW signal transduction; probe: diagnosis; therapy;  
 KW neurodegeneration; neuroproliferation; cancer.

OS Mus sp.

FT Key Location/Qualifiers

FT Peptide 1..28 /label= Sig-peptide

FT Modified-site 64..66 /label= N-glycosylation\_site

FT Modified-site 343..345 /label= N-glycosylation\_site

FT Modified-site 410..412 /label= N-glycosylation\_site

FT Domain 555..579 /label= Transmembrane-domain

PN WO9621013-A1.

PD 11-JUL-1996.

PF 03-JAN-1996; 96WO-US00419.

PR 03-JAN-1995; 95US-0368776.

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 (SUGF-) SUGEN INC.

PI Closek T, Millaer B, Ullrich A;

DR MPI; 1996-333988/33.

DR N-PSDB; AAT32960.

PT New mouse development kinase 1 gene - used for developing prods. for  
 PT diagnosis and treatment of abnormalities in signal transduction  
 PT pathways

PS Example 1; Page 105-108; 128pp; English.

CC Mouse developmental kinase 1 (MDK1) (AAR03421) is a new member of the  
 CC eck/eph family of receptor tyrosine kinases (RTKs). Its amino  
 CC acid sequence was deduced from a cDNA clone (AAT32960) isolated  
 CC from mouse embryo and adult brain libraries. The distinct  
 CC patterns of MDK1 expression during mouse development suggest an  
 CC important role for MDK1 in the formation of neuronal structures.  
 CC MDK1 may be obtd. by expression in host cells. It can be used  
 CC in methods for the diagnosis of diseases characterised by  
 CC abnormality in a signal transduction pathway, such as  
 CC neuroproliferative or neurodegenerative disorders or cancer,  
 CC to screen for (ant)agonists, and to raise antibodies.

SO Sequence 998 AA:

Query Match 4.1%; Score 40; DB 17; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-33;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 775 RMTAPEAIQYRKFTSADVMSYGIYVMEVMSYGERPYNDM 814  
 |||||||  
 DB 801 rvtapeaigrykftsasdvmsygiyvmewmsygerpyndm 840

## RESULT 11

AAR41897  
 ID AAR41897 standard; Protein; 59 AA.

AC AAR41897;

DT 10-MAR-1994 (first entry)

DE Partial bptk1 gene prod.

KW PTK; protein tyrosine kinase; catalytic domain; c-kit; brain;  
 amplification; primer; polymerase chain reaction; PCR.

OS Homo sapiens.

PN WO9315201-A.

PD 05-AUG-1993.

PF 22-JAN-1993; 93WO-US00586.

PR 22-JAN-1992; 92US-0826935.

PA (NENE-) NEW ENGLAND DEACONESS HOSPITAL.

PI Avraham H, Cowley S, Groopman J, Scadden D;

DR WPI; 1993-320330/40.

PT New protein tyrosine kinase genes and proteins encoded by genes -  
 are of human mega-karyocytic origin

PS Claim 7; Fig 9; 60pp; English.

CC PTK genes were identified using two sets of degenerative  
 CC oligonucleotide primers: a first set which amplifies all PTK DNA  
 CC segments (AAQ49743-44), and a second set which amplifies highly  
 CC conserved sequences present in the catalytic domain of the c-kit  
 CC subgroup of PTKs (AAQ49745-46). The PTK genes identified are described  
 CC in AAQ49747-57 and AAR41897-02.  
 CC The bptks are expressed in human brain tissue.

SO Sequence 59 AA;

Query Match 4.0%; Score 39; DB 14; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 733 ARNIIVNSNLVCKVSDFGLSRFLDDTSDPTYSALGK 771  
 |||||||  
 DB 1 arnlvnsnlvckvdsdfiglsrflddtsdptysal9gx 39

## RESULT 12

AAR85924  
 ID AAR85924 standard; Peptide; 59 AA.

AC AAR85924;

DT 14-FEB-1996 (first entry)

XX Protein tyrosine-kinase bptk1 fragment.

KW Protein tyrosine-kinase; PTK; bptk1; agonist; cell growth;  
 differentiation.

OS Homo sapiens.

PN WO9527061-A1.

PD 12-OCT-1995.

PF 04-APR-1995; 95WO-US04228.

PR 04-APR-1994; 94US-0222616.

PA (GETH ) GENENTECH INC.

PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;

PI Wood WI;

DR WPI; 1995-366160/47.

PT Agonist antibodies which activate specific protein tyrosine  
 PT kinase(s) - also activate chimeric proteins of kinase extracellular  
 PT domain and Ig constant domain, useful for studying, and therapeutic  
 PT modulation of, cell growth and differentiation

PS Disclosure; Page 71-72; 125pp; English.

CC DNA probes based on protein tyrosine-kinase (PTK) sequences were used  
 CC to screen cDNA libraries to identify novel PTK genes. The bptks,  
 CC bptk1, bptk2, bptk3, bptk4, bptk5 and bptk7 (AAR85924-28 and AAR85935,  
 CC respectively) are expressed in human brain tissue and show homology  
 CC to known PTKs. These novel PTKs can be used in the design of  
 CC drugs that modulate PTK activity.

SO Sequence 59 AA;

Query Match 4.0%; Score 39; DB 16; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-33;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 733 ARNIIVNSNLVCKVSDFGLSRFLDDTSDPTYSALGK 771  
 |||||||  
 DB 1 arnlvnsnlvckvdsdfiglsrflddtsdptysal9gx 39

## RESULT 13

AAR79141  
 ID AAR79141 standard; Protein; 57 AA.

AC AAR79141;

DT 22-FEB-1996 (first entry)

DE Human receptor type kinase.

XX receptor type kinase; osteoblast; screening; anti-cancer; diagnosis;  
 KW treatment; bone disease.

OS Homo sapiens.

PN JP07155187-A.

PD 20-JUN-1995.

PF 03-DEC-1993; 93JP-0303622.

PR 03-DEC-1993; 93JP-0303622.

PA (ASAH ) ASAH KASEI KOGYO KK.

DR WPI; 1995-250736/33.

DR N-PSDB; AAQ96250.



XX Human receptor tyrosine kinase partial cDNA - used to develop  
PT medicaments for the treatment of bone disease caused by  
XX proliferation of osteoblast cells  
XX  
PS Claim 1: Page 5; 5pp; Japanese.  
CC The human receptor tyrosine kinase was isolated from a human  
CC osteoblastoid cell line (MG63) by reverse transcriptase-polymerase  
CC chain reaction. The gene fragment (AA096249) can be used for the  
CC screening of cells for anti-cancer agents, and for treatment of bone  
CC diseases due to the proliferation of osteoblasts.  
XX  
SQ Sequence 57 AA:

Query Match 3.8%; Score 37; DB 16; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.4e-31;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 NIIVNSNLVCKVSDPGLSRFLEDPTSDPTYSALGK 771  
Db 1 nllvnsnlvckvsgdfglrflcdtsdptysalgyk 37  
|||||

RESULT 14  
AAW79147  
ID AAW79147 standard; Protein: 57 AA.  
XX  
AC AAW79147;  
XX  
DT 19-NOV-1998 (first entry)  
XX  
DE Receptor protein tyrosine kinase (PTK) subtype tyro-5.  
XX  
KM PTK; receptor; protein tyrosine kinase; brain tissue.  
XX  
OS Rattus sp.  
XX  
PM US5811516-A.  
XX  
PD 22-SEP-1998.  
XX  
PF 02-JUN-1995; 95US-0456647.  
XX  
PR 15-MAY-1992; 92US-0884486.  
XX  
PR 02-MAY-1994; 94US-0237401.  
XX  
PR 02-JUN-1995; 95US-0456647.  
XX  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Lai CHC, Lemke GE;  
XX  
DR WPI: 1998-530939/45.  
XX  
DR N-PSDB; AAV55890.  
XX  
XX Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably  
XX expressed in brain tissue  
XX  
XX Example 2: Columns 45-46; 46pp; English.  
XX  
CC This represents a novel receptor protein tyrosine kinase (PTK)  
CC polypeptide subtype tyro-5. The invention provides polynucleotide  
CC sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.  
CC The PTK subtypes are found expressed predominantly in the brain tissue.  
XX  
SQ Sequence 57 AA:

Query Match 3.8%; Score 37; DB 19; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.4e-31;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 NIIVNSNLVCKVSDPGLSRFLEDPTSDPTYSALGK 771  
Db 1 nllvnsnlvckvsgdfglrflcdtsdptysalgyk 37  
|||||

RESULT 15  
AAW81404  
ID AAW81404 standard; Protein: 57 AA.  
XX  
AC AAW81404;  
XX  
DT 22-JAN-1999 (first entry)  
XX  
DE Receptor protein tyrosine kinase (PTK) subtype tyro-5.  
XX  
KM PTK; receptor; protein tyrosine kinase; recombinant; grafting;  
KM diagnosis; tumour; skin transplant; connective tissue; tyro-5.  
XX  
OS Rattus sp.  
XX  
PM US5837448-A.  
XX  
PD 17-NOV-1998.  
XX  
PF 02-MAY-1994; 94US-0237401.  
XX  
PR 15-MAY-1992; 92US-0884486.  
XX  
PR 02-MAY-1994; 94US-0237401.  
XX  
PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
XX  
PI Lai CHC, Lemke GE;  
XX  
DR WPI: 1999-023436/02.  
XX  
DR N-PSDB; AAV65312.  
XX  
PT Nucleic acids encoding protein tyrosine kinase subtypes - for  
PT identification of new subtypes and treatment of diseases associated  
XX with the kinase  
XX  
PS Claim 10: Columns 45-46; 47pp; English.  
XX  
XX This represents a receptor protein tyrosine kinase (PTK) subtype tyro-5.  
XX The invention provides sequences AAV65308 to AAV65313, AAV65315, and  
XX AAV65317 to AAV65319 that encode proteins having a tyrosine kinase domain  
XX and a tissue expression pattern of a receptor PTK subtype selected from  
XX tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10, tyro-11,  
XX and tyro-12, respectively. The polynucleotides are useful for the  
XX detection of tyrosine kinase domain sequences and detection of tissue  
XX expression patterns of PTK subtypes. The cDNAs can also be injected into  
XX oocytes, the protein expressed, and expression products screened for  
XX using antibodies against tyrosine kinase epitopes. These subtypes  
XX sequences can be used for the design of oligonucleotides, for use in  
XX amplification reactions to isolate other subtype sequences. These  
XX detection protocols are used in the diagnosis of diseases associated with  
XX (receptor) PTKs. Recombinant vectors expressing the subtypes can be used  
XX to treat related diseases e.g. tumours, by introduction of the vectors  
XX into skin transplants, then grafting these into the connective tissue of  
XX the dermis, thus specifically targeting tumours as the proteins are  
XX released from the matrix.  
XX  
SQ Sequence 57 AA:

Query Match 3.8%; Score 37; DB 20; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.4e-31;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 735 NIIVNSNLVCKVSDPGLSRFLEDPTSDPTYSALGK 771  
Db 1 nllvnsnlvckvsgdfglrflcdtsdptysalgyk 37  
|||||

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